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OM nucleic - nucleic search, using sw model

Run on: December 22, 2002, 07:41:51 ; Search time 2776 Seconds

(without alignments)
13817.543 Million cell updates/sec

Title: US-09-964-994-1

Perfect score: 1318
Sequence: 1 cagttcttcattctgttaca.....aaaaaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY_NUC
Gapop 10.0 / Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

1 number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	1318	100.0	1318	AX300012	AX300012 Sequence
2	1282.6	97.3	2859	AY040567	AY040567 Homo sapi
3	1280.4	97.1	1351	HSA313162	AJ313162 Homo sapi
4	1094.4	83.0	2367	AX469514	AX469514 Sequence
5	1080.6	82.0	2763	AF040566	AY040566 Homo sapi
6	1078.4	81.8	1255	AX399654	AX399654 Sequence
7	1078.4	81.8	1255	HSA313161	AJ313161 Homo sapi
8	1078.4	81.8	1255	AY044429	AY044429 Homo sapi
9	910	69.0	2271	AX469509	AX469509 Sequence
10	831.6	63.1	2149	AX151700	AX151700 Sequence
11	831.6	63.1	2149	AX179609	AX179609 Sequence
12	805.2	61.1	810	AX399656	AX399656 Sequence
13	730.6	55.4	2593	AY040568	AY040568 Homo sapi
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16	449.2	34.1	750	AX193682	AX193682 Sequence
17	449.2	34.1	750	AX399652	AX399652 Sequence
18	406	30.8	113811	HSJ503F13	AL050337 Human DNA
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22	398.2	30.2	693	AX193707	AX193707 Sequence
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39	67	5.1	1750	AX464054	AX464054 Sequence
40	67	5.1	1801	AX180163	AX180163 Sequence
41	67	5.1	1801	AX180663	AX180663 Sequence
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ALIGNMENTS

RESULT 1
AX300012
LOCUS AX300012
DEFINITION Sequence 17 from Patent WO0166740.
ACCESSION AX300012
VERSION AX300012.1 GI:17129481
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Eaton,D.L., Fong,S., Goddard,A., Godowski,P.J., Grimaldi,C.J.,
Gurney,A.L., Tunas,D., Watanabe,C.K., Wood,W.I. and Zhang,Z.
TITLE Compositions and methods for the treatment of immune related

diseases
Patient: WO 0166740-A 17 13-SEP-2001;
Genentech, Inc. (US)
Location/Qualifiers
1. 1318
/organism="Homo sapiens"
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BASE COUNT 451 a 251 c 259 g 357 t
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Query Match 100.0%; Score 1318; DB 6; Length 1318;
Best Local Similarity 100.0%; Pred. No. 9.8e-274;
Matches 1318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1261 GAGATTAAGTGTCTATGAAAAAATTTGAAAAAATTTGAAAAAATTTGAAAAA 1318
RESULT 2
AY040567 2859 bp mRNA linear PRI 19-AUG-2001
LOCUS
DEFINITION
AY040567 Homo sapiens interleukin 22-binding protein CRF2-10L (IL22BP) mRNA,
complete cds, alternatively spliced.
AY040567.1 GI:15212827
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 2859)
Kotenko,S.V., Izotova,L.S., Miroshchichenko,O.V., Esterova,E.,
Dickensheets,H., Donnelly,R.P. and Pestka,S.
IDENTIFICATION, cloning, and characterization of a novel soluble
receptor that binds IL-22 and neutralizes its activity
J. Immunol. 166 (12), 7096-7103 (2001)
JOURNAL
MEDLINE
21286453
PUBMED
11390454
REFERENCE
AUTHORS
2 (bases 1 to 2859)
Kotenko,S.V. and Pestka,S.
DIRECT SUBMISSION
SUBMITTED (15-JUN-2001) Molecular Genetics and Microbiology,
UMDNJ-Robert Wood Johnson Medical School, 675 Hoes Lane,
Piscataway, NJ 08854-5635, USA
FEATURES
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1. 2859
Location/Qualifiers
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1. 2859
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[illegible]

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Db	907	CTATACGAGAGTTTATATATTAATTAACCAATTCACCTGAAAAAGGAGCAAAAGTTTATGAAAGG	966
QY	901	GCCTACAGAGAGGGTTGGAATTTGAAGCTCTTAACACACACTCCACTACTGTAGTGGCT	960
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QY	961	GAATATATATCAGCCCATGTTAGACAGAAAGTCAGAGAACTGAGAAAGAGATGTGTGGAA	1020
Db	1027	GAATATATATCAGCCCATGTTAGACAGAAAGTCAGAGAACTGAGAAAGAGATGTGTGGAA	1086
QY	1021	ATTCATGACACTTTGGGAATTTGGCATTGACAAATGTGAATTTCTAAAGCTCCCTGGAA	1080
Db	1087	ATTCATGACACTTTGGGAATTTGGCATTGACAAAGTGTGAATTTCTAAAGCTCCCTGGAA	1146
QY	1081	CAGGATGACCTGTGTTGAAGATCTCTTAAATATGTTTGTATTTCTTAAAGCAA	1140
Db	1147	CAGGATGACCTGTGTTGAAGATCTCTTAAATATGTTTGTATTTCTTAAAGCAA	1206
QY	1141	TATTCACGTGTACACCTTGAGGACCTCTTTGTTATTCATTCTTTATCTTATATTTTC	1200
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[illegible]

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VERSION	AY040566.1	GI:15212825
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ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
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JOURNAL	Kotenko,S.V., Izotova,L.S., Mirochnitchenko,O.V., Esterova,E.,	
MEDLINE	Dickensheets,H., Donnelly,R.P. and Pestik,S.	
PUBMED	Identification, cloning, and characterization of a novel soluble	
REFERENCE	J. Immunol. 166 (12), 7096-7103 (2001)	
AUTHORS	2 (bases 1 to 2763)	
TITLE	Kotenko,S.V. and Pestika,S.	
JOURNAL	Direct Submission	
MEDLINE	Submitted (15-JUN-2001) Molecular Genetics and Microbiology,	
PUBMED	UMDNJ-Robert Wood Johnson Medical School, 675 Hoes Lane,	
REFERENCE	Piscataway, NJ 08854-5635, USA	
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REFERENCE	binding of IL-22 to the functional cell surface IL-22	
AUTHORS	receptor complex"	
TITLE	/note="CRF class II member 10; soluble receptor; IL-22BP;	
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PUBMED	/product="interleukin 22-binding protein CRF-10"	
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AUTHORS	/db_xref="GI:15212826"	
TITLE	/translation="MMPKHCFLGLISFLTGVAGTOSTHESLPORVQDSRNPHNIT	
JOURNAL	LQMPGRRLNTSSYFEVKIKIVGQRQWKNEDEWGTOELSDLTSETSDIQEPLYGKR	
MEDLINE	VRAASAGSISEMSMTPEPTWMEKRIIDEPVNINIIQVNGSLIYLHAENLPRYQERKN	
PUBMED	VSIDIEYELIARVFIFINNLSLEKEQRYVEGAHRAVEIALTPHSSCYVAETIQMDLR	
REFERENCE	RSQRSEECVCEIP"	
AUTHORS	BASE COUNT	866 a 479 c 528 g 890 t
TITLE	ORIGIN	
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MEDLINE	Best Local Similarity	92.2%; Pred. No. 1.4e-222;
PUBMED	Matches 1189; Conservative	0; Mismatches 4; Indels 96; Gaps 1;
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Qy	661	AGCTACTAGAAATGAGCATGACGCCGGGGTCACTCCCTGGTGGGAAACAAATAATGAT	720
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Qy	721	CTCTCAGTCATGAATATATAAACCAAGTCAAATGGCTCTTGTGTGTAATTCATGCTCCA	780
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Db	722	AATTTACCATATAGTATACCAAAAGGAAAAAATGATCTATAGAAATTAATATAGACTA	781
Qy	841	CTATACCGAGTTTTATATATTAATTAACAATTCACTAGAAAAAGACAAAAGTTTATGAAGG	900
Db	782	CTATACCGAGTTTTATATATTAATTAACAATTCACTAGAAAAAGACAAAAGTTTATGAAGG	841
Qy	901	GCTCACAGAGCGGTGAANAATGAACTCTAACACCACTCCAGCTACTGTGTGATGGCT	960
Db	842	GCTCACAGAGCGGTGAANAATGAACTCTAACACCACTCCAGCTACTGTGTGATGGCT	901
Qy	961	GAAATATATCAAGCCCATGTTAGACAGAAAGATCAGAGAAGTGAAGAGAGATGTGTGAA	1020
Db	902	GAAATATATCAAGCCCATGTTAGACAGAAAGATCAGAGAAGTGAAGAGAGATGTGTGAA	961
Qy	1021	AATTCATGACTTGTGGAAATTTGGCAATTCAGCAATTCAGAAATTCGAAAGCTCCCGAGAA	1080
Db	962	AATTCATGACTTGTGGAAATTTGGCAATTCAGCAATTCAGAAATTCGAAAGCTCCCGAGAA	1021
Qy	1081	CAGGATGACTCGTGTGTTGAAGAGCTTATATTAATAATGTTTTGTATATTTCTTAAAGCA	1140
Db	1022	CAGGATGACTCGTGTGTTGAAGAGCTTATATTAATAATGTTTTGTATATTTCTTAAAGCA	1081
Qy	1141	TATTCACGTTCACCTGGGAGACTTCTTGTATTCATTCCTTTTATCCTTATATTTTC	1200
Db	1082	TATTCACGTTCACCTGGGAGACTTCTTGTATTCATTCCTTTTATCCTTATATTTTC	1141
Qy	1201	ATTTGTAACATATATTTGAAGACATTCGCCCGGAAAAATGAAATGTAAAGATGAGCA	1260
Db	1142	ATTTGTAACATATATTTGAAGACATTCGCCCGGAAAAATGAAATGTAAAGATGAGCA	1201
Qy	1261	GAGAAATGAAGTGTCTATGAAAAAATAA 1289	
Db	1202	GAGAAATGAAGTGTCTATGAAAAATTCAGAA 1230	

RESULT 6				
AX399654				
LOCUS	AX399654	1255 bp	DNA	PAT 06-JUN-2002
DEFINITION	Sequence 3 from Patent Epi191035.			

ACCESSION	AX399654	GI:21335431
VERSION	AX399654.1	
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 Weiss, B., Sabat, R., Assadullah, K. and Toshi, L.	
JOURNAL	Three members of the cytokin-receptor class II family Patent: EP 1191035-A 3 27-MAR-2002;	
FEATURES	SCHERING AKTENSEBELLSCHAFT (DE)	
source	Location/Qualifiers	
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Query Match	81.8%; Score 1078.4; DB 6; Length 1255;	
Best Local Similarity	92.4%; Pred. No. 4.1e-22;	
Matches 1185; Conservative	0; Mismatches 1; Indels 96; Gaps	
QY	1 CAGTTCTTCATCTCTGTACATCAAAATGAATAAATACCAATCTCTTACACTTCAATAGA	60
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QY	241 ATGCTTAACATATGCTTCTTAGGCTTCCATCAGTTTCTTCTTACTAGTGTAAGAGA	300
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QY	301 ACTCAGTCAAGCATGATCTCTGAAGCGTCAGGGGTACAATTGACGCCGAAATTTT	360
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QY 1141 TATTCACGTATACACCTTGGGACTCTTTGTTTATTCATCTTTATCTTATATTC 1200
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Db 1231 GAGATTAAGTGTCTATGAAA 1252

RESULT 7
HSA313161
LOCUS HSA313161 1255 bp mRNA linear PRI 21-OCT-2001
DEFINITION Homo sapiens mRNA for soluble cytokine class II receptor, short isoform (CRF2-S1 gene).
ACCESSION AJ313161
VERSION AJ313161.1 GI:16304590
KEYWORDS alternative splicing; CRF2-S1 gene; short isoform; soluble cytokine class II receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1255)
AUTHORS Gruendberg, B.H., Schoenemeyer, A., Weiss, B., Toschi, L., Kunz, S., Wolk, K., Asadullah, K. and Sabat, R.
A novel, soluble homologue of the human IL-10 receptor with preferential expression in placenta
JOURNAL Genes Immun. 2 (6), 329-334 (2001)
MEDLINE 21518574
PUBMED 11607789
REFERENCE 2 (bases 1 to 1255)
AUTHORS Weiss, B.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2001) Weiss B., Genomics & Bioinformatics, Schering AG, Muellerstr. 178, Berlin, D-13342, GERMANY
COMMENT Related sequence AJ313162: long isoform.
FEATURES
source Location/Qualifiers
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/chromosome="6"
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1000..1255
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BASE COUNT 402 a 251 c 246 g 356 t
ORIGIN
Query Match 81.8%; Score 1078.4; DB 9; Length 1255;
Best Local Similarity 92.4%; Pred. No. 4.1e-222;
Matches 1185; Conservative 0; Mismatches 1; Indels 96; Gaps 1;
QY 1 CAGTTCTTCATCTGTATACATCAATGATATATATACCATCTCTAGACTTCATAGA 60
Db 67 CAGTTCTTCATCTGTATACATCAATGATATATATACCAATCTCTAGACTTCATAGA 126
QY 61 GGATTAACAAGACAAATATGGGAAAAACATTAACATGGCTCCCATATATTAGACT 120
Db 127 GGATTAACAAGACAAATATGGGAAAAACATTAACATGGCTCCCATATATTAGACT 186
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Db 367 ACTCAGTCAACGATGAGTCTCTGAAGCCTCAGAGGGTACATATTCAGTCCGAAATTT 426
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Db 487 GTGCATACAAATCATGTTCTCTATGACAGATGAAAGCTCTCACACAGACCAAGTGA 500
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QY 541 AGACAAATGGAATAAAGAAAGACTGTTGGGTACTCAAGAACTCTTGTGACCTTACC 600
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Db 505 GTGAACCTCGACATATAGAGACCTTTATACGGAGGAGTGAAGGGCGGCTGGGA 564
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Db 625 CTCAGATCATATATATACCAAGTCAATGGCTCTTTGTGGTAATTCATGCTCCAA 684
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QY 1022 TTCATGACTTTGGAAATTTGGCATTCAGCAATGTGAAATTTAAAGCTCCAGAAC 1081
Db 925 TTCATGACTTTGGAAATTTGGCATTCAGCAATGTGAAATTTAAAGCTCCAGAAC 984
QY 1082 AGGATGACTGTGTGTGAAGATCTTATTTAAATTTGTTTGTATTTTCTTAAAGCAAT 1141
Db 985 AGGATGACTGTGTGTGAAGATCTTATTTAAATTTGTTTGTATTTTCTTAAAGCAAT 1044
QY 1142 ATTCACGTTTACACCTTGGGAGCTTTGTTTATTCATCTTTTATCTTATATTTCA 1201
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Db 1105 TTTGTAACATATATTTGAAGACATTTCCCGGAAATTTGAATTTGAAGATGAGGAG 1164
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Db 1165 AGAATTAAGTGTCTATGAAAAATTCAGAA 1192

RESULT 9
AX469509
LOCUS AX469509 2271 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 5 from Patent WO0224912.
ACCESSION AX469509
VERSION AX469509.1 GI:21901794
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Renaud,J.C. and Dumoutier,L.
TITLE Isolated nucleic acid molecules which encode a soluble IL-11/IL-22
receptor or binding protein which binds to IL-11/IL-22 and uses
thereof
JOURNAL Patent: WO 0224912-A 5 28-MAR-2002.
LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES
source 1..2271
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/db_xref="taxon:9606"
BASE COUNT 709 a 400 c 444 g 718 t
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Query Match 69.0%; Score 910; DB 6; Length 2271;
Best Local Similarity 91.0%; Pred. No. 7,9e-186;
Matches 1019; Conservative 0; Mismatches 5; Indels 96; Gaps 1.
QY 170 CTGTTCTCTTTGGTCTGAGCTGGTTAAAAAGACACTGGTTCCTGAACAGTCAAC 229
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QY 230 TTGCACCATGATGCGCTTAACATTTCTAGGCTTCCTATAGCTTCTCTTACTG 289
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QY 290 GTTAGCAGGAACTCAGTCAACGATGAGTCTGAAACCTCAGAGGCTAGCAATTTCACT 349
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QY 350 CCCGAAATTTTCAACAACTTTTGGCATGAGCTGGAGGAGGCACTTACTGCAACAGCA 409
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QY 530 AATATGACACAGACATATGAAAAATTAAGAACTGTGGGGTACTGACAACTCTCTT 589
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QY 590 GTGACCTTACAGTGAACCTCAGACATACAGAACTTATACGGAGGCTGAGGGGG 649
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Db 486 CAAATATATATCTCCAGTCAATATATATATATATATATATATATATATATATAT 545
QY 770 TCCATGCTCCAAATTTTACATATATATATATATATATATATATATATATATAT 829
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1007 AGAGATGTGTGGAATTTCCATGACTTGTGG 1036
781 AGAGATGTGTGGAATTTCCATGACTTGTGG 810

RESULT 13
LOCUS AY040568 2593 bp mRNA linear PRI 19-AUG-2001
DEFINITION Homo sapiens interleukin 22-binding protein CRF2-10S (IL22BP) mRNA,
complete cds, alternatively spliced.
ACCESSION AY040568
VERSION AY040568.1 GI:15212829
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2593)
Kotenko,S.V., Izotova,L.S., Mirochnitchenko,O.V., Esterova,E.,
Dichensheets,H., Donnelly,R.P. and Pestka,S.
Identification, cloning, and characterization of a novel soluble
receptor that binds IL-22 and neutralizes its activity
J. Immunol. 166 (12), 7096-7103 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
21286453
11390454
2 (bases 1 to 2593)
Kotenko,S.V. and Pestka,S.
Direct Submission
Submitted (15-JUN-2001) Molecular Genetics and Microbiology,
UMDNJ-Robert Wood Johnson Medical School, 675 Hoes Lane,
Piscataway, NJ 08854-5635, USA

AUTHORS
JOURNAL
TITLE
FEATURES
source
1.2593
location/Qualifiers
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BASE COUNT 798 a 448 c 507 g 840 t
Query Match 55.4%; Score 730.6; DB 9; Length 2593;

Best Local Similarity 79.1%; Pred. No. 3,5e-147;
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QY 1 CAGTTTCTTCTCTGTAACATCAAAATGATATATATATACCAATCTCTAGACTCTCATAGA 60
DB 38 CAGTTTCTTCTCTGTAACATCAAAATGATATATATATATACCAATCTCTAGACTCTCATAGA 97
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QY 121 TATTATGACACTAAATATGGCATTTAAATTTACCAAAAGAGACAGCATCTGTTCTCT 180
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DB 732 GAAATATATCAGCCCATGTTAGACAGAGAAGTCAAGAAAGTGAAGAGATGTGTGAA 791
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Db 792 ATTCATGACCTTGGAAATTTGGCATTGACGATGGAATTCATAAGCTCCGAGAA 851
 QY 1081 CAGATGACCTGCTGTTGAAGGATCTTATTAATGTTTGTATTTCTTAAAGCAA 1140
 Db 852 CAGATGACCTGCTGTTGAAGGATCTTATTAATGTTTGTATTTCTTAAAGCAA 911
 QY 1141 TATCCTGTTACCTGTTGGGACCTTTGTTATCCATCTTTATCCCTTATTTTC 1200
 Db 912 TATCCTGTTACCTGTTGGGACCTTTGTTATCCATCTTTATCCCTTATTTTC 971
 QY 1201 ATTTGTAACCTATTTGAAGCAGATCCCGCCGAAATTAAGTAAAGATGAGCA 1260
 Db 972 ATTTGTAACCTATTTGAAGCAGATCCCGCCGAAATTAAGTAAAGATGAGCA 1031
 QY 1261 GGAATTAAGTCTTATGAAAAAATTAAGTAAAGATGAGCA 1289
 Db 1032 GGAATTAAGTCTTATGAAAAAATTAAGTAAAGATGAGCA 1060

RESULT 14
 97262
 DEFINITION Homo sapiens mRNA for Interleukin-22 binding protein (IL-22BP gene).
 ACCESSION HSA297262 775 bp mRNA linear prt 19-DEC-2001
 VERSION AJ297262.1 GI:17974196
 KEYWORDS IL-22BP gene; Interleukin-22 binding protein.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 Dumoutier, L., Lejeune, D. and Renauld, J.C.
 Cloning and characterization of Interleukin-22 Binding Protein (IL-22BP), a natural antagonist of IL-TIF/IL-22
 unpublished
 2 (bases 1 to 775)
 Renauld, J.C.
 Direct Submission
 Submitted (19-DEC-2000) Renauld J.C., UCL 74.59, Ludwig Institute for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels, Belgium
 FEATURES
 source location/Qualifiers
 1. 775
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /tissue_type="breast"
 22. 717
 /gene="IL-22BP"
 22. 717
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 /codon_start=1
 /product="Interleukin-22 binding protein"
 /protein_id="CAC83097.1"
 /db_xref="GI:17974197"

gene
 CDS
 22. 717
 /gene="IL-22BP"

BASE COUNT 248 a 157 c 175 g 195 t
 ORIGIN

Query Match 50.8% Score 669; DB 9; Length 775;
 Best Local Similarity 89.0%; Pred. No. 6.7e-134;
 Matches 775; Conservative 0; Mismatches 0; Indels 96; Gaps 1;
 QY 217 TGAACAGTCACTTGCACATGATGCTTAACATGCTTCTAGCTTCCATCAGT 276
 Db 1 TGAACAGTCACTTGCACATGATGCTTAACATGCTTCTAGCTTCCATCAGT 60
 QY 277 TTTCTCTACTGTTGTTAGCAGAACTAGTCAACGATGAGTCTCTGAGGCTCAGAG 336
 |||||||

Db 61 TTTCTCTACTGTTGTTAGCAGAACTAGTCAACGATGAGTCTCTGAGGCTCAGAG 120
 QY 337 GACATATTCAGTCCCGAAATTTTCAACATTTTGCATATGAGGCTGGAGGCACTT 396
 Db 121 GTCATATTCAGTCCCGAAATTTTCAACATTTTGCATATGAGGCTGGAGGCACTT 180
 QY 397 ACTGGCAACAGCAGTCTATTTTGTGAGTACCAATATCATGTTTCATGACAGATGAAA 456
 Db 181 ACTGGCAACAGCAGTCTATTTTGTGAGTACCAATATCATGTTTCATGACAGATGAAA 218
 QY 457 AGCTCTACACGAGACCAAGTGAATGCTGGCAGACATTTCTGTAACTTCCAGGCTGC 516
 Db 219
 QY 517 AGACATTTGGCTAAATATGAGCAGACAGATGGAATTAAGAGACTGTTGGGCTACT 576
 Db 219
 QY 577 CAAGACTCTCTTGTGACCTTAACAGATGAACCTCAGACATGAGAACTTATTAAGGG 636
 Db 265 CAAGACTCTCTTGTGACCTTAACAGATGAACCTCAGACATGAGAACTTATTAAGGG 324
 QY 637 AGGTGAGAGGGGCGCTGGGAGCTTACATGAGATGAGCATGACGCGGCTTCACT 696
 Db 325 AGGTGAGAGGGGCGCTGGGAGCTTACATGAGATGAGCATGACGCGGCTTCACT 384
 QY 697 CCTGTGGGGAACAAAATATGATCTCCAGTCAATGATATTAACCAAGTCAATGGCTCT 756
 Db 385 CCTGTGGGGAACAAAATATGATCTCCAGTCAATGATATTAACCAAGTCAATGGCTCT 444
 QY 757 TTTGTGTAATTCCTCCATGCTCCCAATTTACCATATGATACCAAGGAAAAAATGTA 816
 Db 445 TTTGTGTAATTCCTCCATGCTCCCAATTTACCATATGATACCAAGGAAAAAATGTA 504
 QY 817 TCTATGAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 876
 Db 505 TCTATGAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 564
 QY 877 AAGGACAAAAGGTTTATGAGAGGGCTCAGAGAGCGGTTGAAATTTGAAGCTTAACACA 936
 Db 565 AAGGACAAAAGGTTTATGAGAGGGCTCAGAGAGCGGTTGAAATTTGAAGCTTAACACA 624
 QY 937 CACTCCAGTACTGTGAGAGGCTGAAATATATGAGGCTTATGAGAGAGAGTCTAG 996
 Db 625 CACTCCAGTACTGTGAGAGGCTGAAATATATGAGGCTTATGAGAGAGAGTCTAG 684
 QY 997 AGAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1056
 Db 685 AGAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 744
 QY 1057 GGAATTTCAAGCTCCCTGAGAGACGAGATG 1087
 Db 745 GGAATTTCAAGCTCCCTGAGAGACGAGATG 775

RESULT 15
 AX193705 696 bp DNA linear PAT 15-AUG-2001
 LOCUS AX193705
 DEFINITION Sequence 27 from Patent WO0136467.
 ACCESSION AX193705
 VERSION AX193705.1 GI:15211554
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 696)
 Gorman, D.M.
 Mammalian receptor proteins: related reagents and methods
 Patent: WO 0136467-A 27 25-MAY-2001;
 JOURNAL SCHERING CORPORATION (US)
 TITLE location/Qualifiers
 1. 696
 source

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OM nucleic - nucleic search, using sw model

Run on: December 22, 2002, 06:48:36 ; Search time 252 Seconds

(without alignments)
11778.309 Million cell updates/sec

Title: US-09-964-994-1

Perfect score: 1318

Sequence: 1 cagttcttcacgttaaca.....aaaaaaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

1 number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1318	100.0	1318	22	AAS15368
2	1094.4	83.0	2367	24	ABK50080
3	1079	81.9	1389	24	ABK70017
4	1078.4	81.8	1255	24	AA146000
5	910	69.0	2271	24	ABK50076
6	831.6	63.1	2149	22	AAD059745
7	831.6	63.1	2149	22	AAF83735
8	805.2	61.1	810	24	AA146001
9	792	60.1	792	24	AAD27816

10	590	44.8	696	24	AAD27815	Human cytokine rec
11	588.4	44.6	696	22	AAD06414	Human DNAX cytokin
12	533	40.4	645	24	AAD27814	Human cytokine rec
13	449.2	34.1	750	22	AAD06410	Human DNAX cytokin
14	449.2	34.1	750	22	AA145999	Human cytokine rec
15	398.2	30.2	693	22	AAD06415	Human DNAX cytokin
16	398.2	30.2	693	22	AAF83736	Human cytokine rec
17	319.6	24.2	747	22	AAD06411	Human DNAX cytokin
18	269.8	20.5	526	22	AAD06416	Human DNAX cytokin
19	197.8	15.0	298	24	AA146018	Human DNAX cytokin
20	171.4	13.0	478	22	ABAS5915	Rat cytokine recep
C 21	171.4	13.0	528	22	ABAS04167	Human foetal liver
22	171.4	13.0	528	22	ABAS59679	Human genome-deriv
23	171.4	13.0	528	22	ABAS28821	Human foetal liver
24	171.4	13.0	528	22	AAK07949	Probe #6687 for ge
25	171.4	13.0	528	22	AAK33818	Human brain expres
26	171.4	13.0	528	22	AA116545	Human bone marrow
27	171.4	13.0	528	22	AA139544	Probe #6478 for ge
28	171.4	13.0	528	22	ABAS08670	Probe #8230 used t
29	170	12.9	170	22	ABAS72221	Human genome-deriv
30	170	12.9	170	22	ABAS38101	Human foetal liver
31	170	12.9	170	22	AAK20644	Probe #16567 for g
32	170	12.9	170	22	AAK46787	Human brain expres
33	170	12.9	170	22	AA125742	Human bone marrow
34	170	12.9	170	22	AA152626	Probe #15675 used
35	170	12.9	170	22	ABAS21105	Human genome-deriv
36	166.2	12.6	390	22	AAD06417	Human DNAX cytokin
C 37	128	9.7	128	22	ABAS68503	Human foetal liver
C 38	128	9.7	128	22	ABAS16694	Human genome-deriv
39	75.4	5.7	1806	22	AAH07662	Mouse cDNA encodin
40	75.4	5.7	1806	22	AAH22834	Mouse IL-20 recept
41	75.4	5.7	1806	24	ABK96195	DNA encoding mouse
42	71	5.4	350	23	ABV57072	Human prostate exp
C 43	70	5.1	348	22	AA110133	Human breast cance
44	67.2	5.1	309	22	ABV44994	Human prostate exp
45	67	5.1	1720	22	AAH07675	Human IL-20RA/immu

ALIGNMENTS

RESULT 1
ID AAS15368 standard; cDNA, 1318 BP.
XX AAS15368;
XX 16-JAN-2002 (first entry)
XX cDNA encoding human PRO19598 polypeptide.
DE Human; PRO19598; clone DN145887; immune-related disorder;
KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
KW neoplasia; transplantation associated disease; gene therapy;
KW immunosuppressive; anti-inflammatory; antidiabetic; ss.
XX Homo sapiens.
XX
XX key Location/Qualifiers
XX CDS 241..1029
XX FT /tag= a
XX FT /product= "PRO19598 polypeptide"
XX FT sig_peptide 241..300
XX FT mat_peptide 301..1026
XX FT /tag= b
XX FT /tag= c
XX WO20016740-A2.
XX 13-SEP-2001.
XX 01-MAR-2001; 2001WO-US06666.

XX 03-MAR-2000; 2000US-187202P.
 PR 21-MAR-2000; 2000US-191015P.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 05-JUN-2000; 2000US-209832P.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 01-DEC-2000; 2000WO-US32678.

XX (GENETECH INC.

XX Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Tunas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI: 2001-625876/72.
 XX P-PSDB: AAU09186.

XX Nucleic acids encoding PRO polypeptides, useful for detecting and
 PR treating immune related diseases and disorders in mammals including
 PR autoimmune diseases, inflammatory diseases and asthma

Claim 2: Fig 17; 122pp; English.

CC The present invention relates to the isolation of 9 novel human PRO
 CC polypeptides (AAU09178-AAU09186) and the cDNA sequences encoding them.
 CC The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,
 CC PRO3151, PRO4372, PRO9964, PRO10008 and PRO19598. The cDNA sequences
 CC encoding these PRO polypeptides have been designated as clones
 CC DNA6886-1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA82773,
 CC DNA92223-2567, DNA101921 and DNA145887 respectively.
 CC Compositions (e.g. vaccines) containing PRO polypeptides and methods of
 CC using these compositions are useful in the treatment and diagnosis of
 CC immune-related disorders. Such disorders include immune-mediated
 CC inflammatory disorders (e.g. osteoarthritis), non-immune-mediated
 CC inflammatory disorders (e.g. diabetes mellitus), infectious disorders
 CC (e.g. granulomatous hepatitis), immunodeficiency disorders (e.g. AIDS),
 CC autoimmune disorders (e.g. rheumatoid arthritis), immune-related renal
 CC diseases (e.g. cirrhosis), demyelinating diseases of the peripheral or
 CC central nervous system (e.g. Guillain-Barre syndrome), immune-mediated
 CC skin diseases (e.g. contact dermatitis), neoplasias and transplantation
 CC associated diseases. The polynucleotide sequences of the invention may
 CC be used in gene therapy. AAS15360-AA15368 represent cDNA sequences
 CC encoding for the novel human PRO polypeptides of the invention.

XX Sequence 1318 BP; 451 A; 251 C; 259 G; 357 T; 0 other;

Query Match 100.0%; Score 1318; DB 22; Length 1318;
 Best Local Similarity 100.0%; Pred. No. 5.3e-263;

Matches 1318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CAGTTCTTCATCTGTAACATCAATGAATATATACCAATCTCTGACTTCAAGA 60
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 1 CAGTTCTTCATCTGTAACATCAATGAATATATACCAATCTCTGACTTCAAGA 60
 61 GGATTTAACAAGACAAATATGGAAGAAACATTAACATGCGTCCCATATTTATGATCT 120
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 61 GGATTTAACAAGACAAATATGGAAGAAACATTAACATGCGTCCCATATTTATGATCT 120
 61 GGATTTAACAAGACAAATATGGAAGAAACATTAACATGCGTCCCATATTTATGATCT 120
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 121 TATTTATGACACTAAATGGATTAATTAATTCACAAAGAGAGAGCAATGTTCCCTCT 180
 181 TTGCTCTGAGCTGTTAAAGAAAGCACTGTTGCTGACAGCTGACACTTGCACACATG 240
 181 TTGCTCTGAGCTGTTAAAGAAAGCACTGTTGCTGACAGCTGACACTTGCACACATG 240
 181 TTGCTCTGAGCTGTTAAAGAAAGCACTGTTGCTGACAGCTGACACTTGCACACATG 240
 181 TTGCTCTGAGCTGTTAAAGAAAGCACTGTTGCTGACAGCTGACACTTGCACACATG 240
 241 ATGCTTAACAATGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
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QY 361 CACAACTTTTTCATTTGGCAGCCTGGAGGCACTTACTGCGACAGCAGCTGCTATTTT 420
 DB 361 CACAACTTTTTCATTTGGCAGCCTGGAGGCACTTACTGCGACAGCAGCTGCTATTTT 420
 QY 421 GTGCACTCAAAATCATGTTCTCATGACACATGAAAAGCTCTCACCAGAACCCAACTGGA 480
 DB 421 GTGCACTCAAAATCATGTTCTCATGACACATGAAAAGCTCTCACCAGAACCCAACTGGA 480
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 QY 541 AGACATGGAATAATTAAGACAGCTGTTGGGTACTCAGAACTCTCTGTGACTTACC 600
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 DB 661 AGCTACTCAGAAATGAGCATGACGCGCGGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
 QY 721 CCTCAGTCAATATATACCAAGTCAATGCTCTTGTGTAATTCATCTGCTCA 780
 DB 721 CCTCAGTCAATATATACCAAGTCAATGCTCTTGTGTAATTCATCTGCTCA 780
 QY 781 AATTTTCCATATATATACCAAGTCAATGCTCTTGTGTAATTCATCTGCTCA 840
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 QY 841 CTAATCCGAGTCTTCTTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
 DB 841 CTAATCCGAGTCTTCTTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
 QY 901 GCTCAGAGGCGGTTGAATGGAAGCTTACACCACTCAGTCTGTAAGTGGCT 960
 DB 901 GCTCAGAGGCGGTTGAATGGAAGCTTACACCACTCAGTCTGTAAGTGGCT 960
 QY 961 GAAATATATCAGCCCATGTTAGACAGAAAGTCAAGAAAGTGAAGATGTGTGGA 1020
 DB 961 GAAATATATCAGCCCATGTTAGACAGAAAGTCAAGAAAGTGAAGATGTGTGGA 1020
 QY 1021 ATTTCATGCTTGTGAATTTGCAATTCAGCAATGGAATTTCTAAAGCTCCCTGAGAA 1080
 DB 1021 ATTTCATGCTTGTGAATTTGCAATTCAGCAATGGAATTTCTAAAGCTCCCTGAGAA 1080
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 DB 1141 TATTCAGTGTACACTTGGGAGCTCTTGTATTCATCTTCTTATTCCTTTATTTTC 1200
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 QY 1261 GAGAAATAAAGTGTCTATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1318
 DB 1261 GAGAAATAAAGTGTCTATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1318

RESULT 2

ABK50080

ABK50080 standard; DNA; 2367 BP.

15-JUL-2002 (first entry)

	DNA encoding human IL-TIF/IL-22 binding protein #2.
KM	Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
XN	IL-TIF/IL-22 antagonist; gene; ds.
XX	
OS	Homo sapiens.
FH	Key Location/Qualifiers
PD	CDS 110..900
Pf	/tag= "a"
	/product= "human IL-TIF/IL-22 binding protein #2"
	/note= "this sequence can optionally start at position 113"
PN	WO200224912-A2.
PP	21-SEP-2001; 2001WO-US29576.
PR	22-SEP-2000; 2000US-234583P. 03-NOV-2000; 2000US-245495P. 31-JUL-2001; 2001US-091916Z.
PA	(LUDW-) LUDWIG INST CANCER RES.
PI	Renaud J, Dumoutier L; MPI: 2002-383190/41. P-PsDB: AAD80324.
DR	
XX	
Pt	Polynucleotide and polypeptide of soluble protein which binds to interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a cell -
PS	Claim 1; Page 40-41; 42pp; English.
XX	
CC	The present invention relates to a new polynucleotide that encodes a soluble protein which binds to Interleukin (IL)-TIF/IL-22 (also referred to as IL-42BP), where the complementary sequence of the Invention hybridizes under stringent conditions to a nucleotide sequence of 2271 or 2366 base pairs, as given in the specification. The molecules of the Invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22 on a cell, for determining whether IL-TIF/IL-22 is present in a sample, for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably <i>in vitro</i> , and for obtaining an antibody molecule specific for the soluble binding protein of the invention, from a population or panel of antibody molecules of diverse binding specificity. The soluble protein is further useful in manufacture of a medicament for treating an IL-22 mediated disease and for assaying an agent, preferably an antibody or a peptide fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding of the soluble protein to IL-TIF/IL-22, where the agent identified is used in the manufacture of medicament for treating IL-TIF/IL-22 mediated disorder. The antibody is useful for determining presence of the soluble protein, where the antibody is detectably labelled. The present nucleic acid sequence encodes the human IL-TIF/IL-22 binding protein #2 of the invention.
SQ	Sequence 2367 BP; 735 A; 425 C; 465 G; 742 T; 0 other:
OY	Query Match 83.0%; Score 1094.4; DB 24; Length 2367; Best Local Similarity 98.6%; Pred. No. 9.3e-217; Matches 1104; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Db	170 CTGTTCTCTTGTCGTGAAGCGTAGTAAGAACAACACTGGTTGCCATCAACAGTCACAC 229 42 CAGTTTCTCTTTGCTCTGAGCTGTAAAGAACACTGGTTCCGTGAACAGTCACAC 101
OY	230 TTGCACCATTGAGCTAATAACATTCCTTTAGAGCTTCCTCATCACATTTCTTCTTACG 289 Dn 102 TTGCACCATTGAGCTAATAACATTCCTTTAGAGCTTCCTCATCACATTTCTTCTTACG 161
OY	290 GTTAGACGAACATCAAGCAACGCACTAGAGTCTCTGAAGCTTCAGAGGCTACAAATTTCACT 349

Db	162	GTGTGACAGAGACTCGATCAACGCGATGAGTCTGTGAAGCCTCAGAGGGTTCAAATTTCACT	221
QY	350	CCCGAAATTTTCCACAACATTTTGGCAATGGCAGCTGGGAGGGCATTACTGGCAACAGA	409
Db	222	CCCGAAATTTTCCACAACATTTTGGCAATGGCAGCTGGGAGGGCATTACTGGCAACAGA	281
QY	410	GTGTCTATTTTGTGAGTACAAAATCATGTTCTCATGACAGTCAAAAGGCTCCACAGA	469
Db	282	GTGTCTATTTTGTGAGTACAAAATCATGTTCTCATGACAGTCAAAAGGCTCCACAGA	341
QY	470	ACCCAATGGGATGCTGCGACACATTTCTGTAACTTCCAGGCTGCAGAACTTGGCTA	529
Db	342	GCCAAAGTGATGCTTGGCAGCACATTTCTTGTAACTTCCAGGCTGCAGAACTTGGCTA	401
QY	530	AATATGGACAGAGCAATGAGAAAAATAAAGAGAGCTGGGGGTACTCAAGACTCTCTT	589
Db	402	AATATGGACAGAGCAATGAGAAAAATAAAGAGAGCTGGGGGTACTCAAGACTCTCTT	461
QY	590	GTGACCTTACCAAGTGAACCTCAGACATACAGAACTTATTAACGGAGGGGTAGGGCG	649
Db	462	GTGACCTTACCAAGTGAACCTCAGACATACAGAACTTATTAACGGAGGGGTAGGGCG	521
QY	650	CCTCGGCGTGGAGCTACTCAAAATGGAGCATGACCGCGGTTCACTCCCTGTGGGAAA	709
Db	522	CCCTGGCGTGGAGCTACTCAAAATGGAGCATGACCGCGGTTCACTCCCTGTGGGAAA	581
QY	710	CAAAATATGATCTCTCCAGTCAATTAATTAACCCAGTCATGGCTCTTGTGGTAAATC	769
Db	582	CAAAATATGATCTCTCCAGTCAATTAATTAACCCAGTCATGGCTCTTGTGTGTAATC	641
QY	770	TCCATGCTCCAAATTTACCATATATAGATACCAAAAGAAAAATGTATCTATAGAGATT	829
Db	642	TCCATGCTCCAAATTTACCATATATAGATACCAAAAGAAAAATGTATCTATAGAGATT	701
QY	830	ACTATGACTCTCTTACCGAGTTTATTAATTAACATTTACTAGAAAAAGGACCAAGCG	889
Db	702	ACTATGACTCTCTTACCGAGTTTATTAATTAACATTTACTAGAAAAAGGACCAAGCG	761
QY	890	TTTATGAAGGGGCTCACAGACGGTTAAATTAAGCTCTTAACACACACTCCAGTACT	949
Db	762	TTTATGAAGGGGCTCACAGACGGTTAAATTAAGCTCTTAACACACACTCCAGTACT	821
QY	950	GTGTAGTGGCTGAATATATATACGCCATGTTAGACAGAGAGTCAAGAGTGAAGAGA	1009
Db	822	GTGTAGTGGCTGAATATATATACGCCATGTTAGACAGAGAGTCAAGAGTGAAGAGA	881
QY	1010	GATGCTGGAATTCCTCAATGACTTGTGAATTTGGCAATTCGCAATGTGGAATTTCAAG	1066
Db	882	GATGCTGGAATTCCTCAATGACTTGTGAATTTGGCAATTCGCAATGTGGAATTTCAAG	941
QY	1070	CTCCCTGGAACAGAGATGACTCGTGTGTGAAGGATCTTATTTAAATGTTTTGTATT	1123
Db	942	CTCCCTGGAACAGAGATGACTCGTGTGTGAAGGATCTTATTTAAATGTTTTGTATT	1001
QY	1130	TCTTAAAGCAATATTCCTACTGTTACACCTTGGGAGCTCTTGTATTCATTCTTTATTC	1186
Db	1002	TCTTAAAGCAATATTCCTACTGTTACACCTTGGGAGCTCTTGTATTCATTCTTTATTC	1061
QY	1190	CTTATATTTTCATTTGTAAACTATATTTGAACACATTCCTCCCGGAAATTTGAATGTA	1245
Db	1062	CTTATATTTTCATTTGTAAACTATATTTGAACACATTCCTCCCGGAAATTTGAATGTA	1121
QY	1250	AAGATGAGCGAGAGATTAAGTGTCTATGAAAAAATAA 1289	
Db	1122	AAGATGAGCGAGAGATTAAGTGTCTATGAAAAATTCAGAA 1161	

XX 15-JUL-2002 (first entry)
 XX CDNA encoding human Pro peptide #57.
 DE
 XX
 XX Human; ss: gene: PRO; secreted protein; transmembrane protein;
 KW genetic disorder; tumour; cancer.
 XX Homo sapiens.
 OS
 XX WO200224888-A2.
 PN
 XX 28-MAR-2002.
 PD
 XX 29-AUG-2001; 2001WO-US27099.
 PF
 XX 01-SEP-2000; 2000US-229896P.
 PR 05-SEP-2000; 2000US-230621P.
 PR 22-SEP-2000; 2000US-235147P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 12-JAN-2001; 2001US-261878P.
 PR 16-JAN-2001; 2001US-261910P.
 PR 16-JAN-2001; 2001US-261939P.
 PR 16-JAN-2001; 2001US-262150P.
 PR 25-JAN-2001; 2001US-264395P.
 PR 02-FEB-2001; 2001US-266421P.
 PR 09-FEB-2001; 2001US-267623P.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 09-MAR-2001; 2001US-274399P.
 PR 03-APR-2001; 2001US-280982P.
 PR 04-APR-2001; 2001US-282129P.
 PR 09-MAY-2001; 2001US-290589P.
 PR 25-MAY-2001; 2001WO-US17802.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 PI WPI: 2002-362426/39.
 DR P-SDB: ABG34086.
 XX
 XX New PRO polypeptides and polynucleotides encoding the polypeptides,
 PI useful in gene therapy, chromosome identification, tissue typing, or
 PI for genetic analysis of individuals with genetic disorders -
 XX
 XX Claim 2; Figure 113; 218pp: English.
 XX
 XX This invention relates to the CDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The
 CC invention also comprises a method for producing the proteins of the
 CC invention by recombinant means and antibodies specific for the PRO
 CC of the invention. The antibody may be used for detecting the PRO
 CC proteins of the invention and may be used to modify their activity.
 CC polynucleotides may be used as hybridisation probes for a CDNA library
 CC to isolate the full-length PRO CDNA or to isolate other cDNAs, to
 CC construct hybridisation probes for mapping the gene which encodes that
 CC PRO and for genetic analysis of individuals with genetic disorders, in
 CC assays to identify other proteins or molecules involved in binding
 CC reaction, to generate transgenic animals or knock-out animals which in
 CC turn are useful in the development and screening of therapeutically
 CC useful reagents, for chromosome identification, and tissue typing. The
 CC PRO polypeptides are useful in gene therapy, and as molecular weight
 CC markers for protein electrophoresis purposes. The sequences may
 CC also be used to detect overexpression on PRO polypeptides in cancerous
 CC tumours and for screening for differentially expressed genes using
 CC microarray technology. The present sequence represents a CDNA encoding

CC a human PRO protein of the invention.
 XX
 XX Sequence 1389 BP; 460 A; 269 C; 260 G; 400 T; 0 other:
 S0
 Query Match 81.9%; Score 1079; DB 24; Length 1389;
 Best Local Similarity 92.2%; Pred. No. 1.3e-213;
 Matches 1188; Conservative 0; Mismatches 5; Indels 96; Gaps 1;
 QY 1 CAGTTCTTCATCTGTACATCAATGATTAATTAATACCAATCTCCAGCTCATACAGA 60
 DB |
 DB 63 CAGTTCTTCATCTGTACATCAATGATTAATTAATACCAATCTCCAGCTCATACAGA 122
 QY 61 GGATTACAAAGCAAAATATGGAAGAAACATACATGGCCCATTAATTATAGATCT 120
 DB |
 DB 123 GGATTACAAAGCAAAATATGGAAGAAACATACATGGCCCATTAATTATAGATCT 182
 QY 121 TATTTATGACACTAAATGACATTAATTAATTAATTAATTAATTAATTAATTAAT 180
 DB |
 DB 183 TATTTATGACACTAAATGACATTAATTAATTAATTAATTAATTAATTAATTAAT 242
 QY 181 TTGGTCTGAGCTGTTAAAGGAAACATGCTGCTGGAACAGTCACTTGAACCATG 240
 DB |
 DB 243 TTGGTCTGAGCTGTTAAAGGAAACATGCTGCTGGAACAGTCACTTGAACCATG 302
 QY 241 ATGCCATAACATTTCTTCTAGGCTTCTCATCATGATTTCTTCTTACTGATGACAGA 300
 DB |
 DB 303 ATGCCATAACATTTCTTCTAGGCTTCTCATCATGATTTCTTCTTACTGATGACAGA 362
 QY 301 ACTCAGTCAACGATGATGCTCTGAAAGCCCTCAAGAGGTACAAATTTGATCCGAAATTT 360
 DB |
 DB 363 ACTCAGTCAACGATGATGCTCTGAAAGCCCTCAAGAGGTACAAATTTGATCCGAAATTT 422
 QY 361 CACAAATTTTGGCAATGGCAGCCTGGAGGAGCACTTACTGGCAACAGCACTGATTTT 420
 DB |
 DB 423 CACAAATTTTGGCAATGGCAGCCTGGAGGAGCACTTACTGGCAACAGCACTGATTTT 482
 QY 421 GTGCAGTACAAATCATGTTCTCATGAGCATGAAAGCTCTCACCAAGCAAGTGA 480
 DB |
 DB 483 GTGCAGTACAAATCATGTTCTCATGAGCATGAAAGCTCTCACCAAGCAAGTGA 496
 QY 481 TGCTGGCAGCAGCATTTCTTCTTAATCTCCAGGCTGCAGAAACATTTGCTAATATGACAG 540
 DB |
 DB 497 -----ATATGACAG 506
 QY 541 AGCAATGGAATAATTAAGAAAGCTGTGGGATCTCAAGAACTCTTGTGACCTTACC 600
 DB |
 DB 507 AGCAATGGAATAATTAAGAAAGCTGTGGGATCTCAAGAACTCTTGTGACCTTACC 566
 QY 601 AGTGAACCTCAGACATACAGAACTTATTAAGGAGGAGGAGGCGGCTGGG 660
 DB |
 DB 567 AGTGAACCTCAGACATACAGAACTTATTAAGGAGGAGGAGGCGGCTGGG 626
 QY 661 AGCTACTCAGAAATGAGCAATGAGCCCGGCTGCCTCCCTGGTGGGAAACAAATATGAT 720
 DB |
 DB 627 AGCTACTCAGAAATGAGCAATGAGCCCGGCTGCCTCCCTGGTGGGAAACAAATATGAT 686
 QY 721 CCTCAGTCTGATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
 DB |
 DB 687 CCTCAGTCTGATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 746
 QY 781 AATTTACATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
 DB |
 DB 747 AATTTACATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 806
 QY 841 CTATACCGAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
 DB |
 DB 807 CTATACCGAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 866
 QY 901 GCTCAGACAGCGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960
 DB |
 DB 867 GCTCAGACAGCGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 926
 QY 961 GAAATATATATGACCCATGTTAGACAGAAAGATCAGAAAGTGAAGAGATGTGTGAA 1020

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Db 927 GAATATATCAGCCAGTTAGACAGAGAAGTCAGAGAAAGATGTCGAA 986
QY 1021 ATCCATGACTTGGAAATGGGATTCAGCAATGGAAATTTAAAGTCCCTGAGAA 1080
Db 987 ATCCATGACTTGGAAATGGGATTCAGCAATGGAAATTTAAAGTCCCTGAGAA 1046
QY 1081 CAGAGTACTGCTGTTGAAGATCTTATTTAAATGTTTGTATTTCTTAAAGCA 1140
Db 1047 CAGAGTACTGCTGTTGAAGATCTTATTTAAATGTTTGTATTTCTTAAAGCA 1106
QY 1141 TATTCACGTGTACCTTGGGACCTCTTGTATTCATCTTTATCTTATATTC 1200
Db 1107 TATTCACGTGTACCTTGGGACCTCTTGTATTCATCTTTATCTTATATTC 1166
QY 1201 ATTTGAACTATATTTGAAGCATTCCTCCCGGAAATTTGAATGTAAGATGAGCA 1260
Db 1167 ATTTGAACTATATTTGAAGCATTCCTCCCGGAAATTTGAATGTAAGATGAGCA 1226
QY 1261 GAGATTAAGTCTTCTATGAAAAA 1289
Db 1227 GAGATTAAGTCTTCTATGAAATTCAGAA 1255

RESULT 4
AL46000
ID AL46000 standard; cDNA; 1255 BP.
AC
AA46000;
DT 08-AUG-2002 (first entry)
DE Human cytokine receptor variant 2 coding sequence.
XX
XX
XX
KW Human cytokine receptor; immune disease; psoriasis; cancer; infection;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW immunosuppressive; antineoplastic; antiarthritic; neuroprotective;
KW antiinflammatory; antitumor; cytostatic; dermatological;
KW chromosome 6q24.1-25.2; receptor; gene; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 304..999
FT /tag=a
FT /product="cytokine receptor variant 2"

EPI191035-A2.
PD 27-MAR-2002.
PE 24-AUG-2001; 2001EP-0250307.
XX
XX
PR 25-SEP-2000; 2000DE-1048626.
PR 17-NOV-2000; 2000DE-1058907.
PR 19-DEC-2000; 2000DE-1064906.
PA (SCHD ) SCHERING AG.
XX
XX
PI Weiss B, Sabat R, Assadullah K, Toshi L;
DR WPI: 2002-333210/37.
DR P-PSDB; AAO17381.
XX
XX
PT New nucleic acid encoding soluble cytokine receptor, useful for
PT diagnosis and treatment of e.g. immune disease, also related protein
PT and antibodies -
XX
XX
XX Claim 1; Page 13; 21pp; German.
CC The present invention provides the protein and coding sequences of 3
CC variants of a human cytokine receptor. The sequences can be used in the

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CC diagnosis, prevention and treatment of immune diseases, including
CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
CC transplant rejection and in reproductive medicine, e.g. for diagnosing
CC abnormal immune reactions which cause abortions. The present sequence is
CC the coding sequence of variant 2 of the invention.
XX
SQ Sequence 1255 BP; 402 A; 251 C; 246 G; 356 T; 0 other;
Query Match 81.8%; Score 1078.4; DB 24; Length 1255;
Best Local Similarity 92.4%; Pred. No. 1.6e-213;
Matches 1185; Conservative 0; Mismatches 1; Indels 96; Gaps 1;
QY 1 CAGTTCCTTCATCTGTACATCAATGAATTAATATCAATCTCTAGACTCATTAAGA 60
Db 67 CAGTTCCTTCATCTGTACATCAATGAATTAATATCAATCTCTAGACTCATTAAGA 126
QY 61 GGATTAACAAAGCAAAATATGGGAAAAACATACATGGGCTGCCATTAATTATGATCT 120
Db 127 GGATTAACAAAGCAAAATATGGGAAAAACATACATGGGCTGCCATTAATTATGATCT 186
QY 121 TATTTATGACACTAAATATGCAATTAATTAACAAAGAGACACATCTGTTCTCT 180
Db 187 TATTTATGACACTAAATATGCAATTAATTAACAAAGAGACACATCTGTTCTCT 246
QY 181 TTGGTCTGAGCTGTTAAAGAACACTGTTGCTGTAACAGTCACTTGCACCATG 240
Db 247 TTGGTCTGAGCTGTTAAAGAACACTGTTGCTGTAACAGTCACTTGCACCATG 306
QY 241 ATGCTTAACATCTGCTTCTAGGCTTCTCATACATGTTCTTCTCTGCTGTAAGAGA 300
Db 307 ATGCTTAACATCTGCTTCTAGGCTTCTCATACATGTTCTTCTCTGCTGTAAGAGA 366
QY 301 ACTAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGTCACAAATTTCCGCAATTTT 360
Db 367 ACTAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGTCACAAATTTCCGCAATTTT 426
QY 361 CACACATTTTGCATTTGCGAGCCTGGAGGAGCTTACTGGAACAGCAGTGTATTTT 420
Db 427 CACACATTTTGCATTTGCGAGCCTGGAGGAGCTTACTGGAACAGCAGTGTATTTT 486
QY 421 GTGAGTCAAAATCATGTTCTCATGCAATGAAGGCTCACCAGAAAGCAAGTGA 480
Db 487 GTGAGTCAAAATCATGTTCTCATGCAATGAAGGCTCACCAGAAAGCAAGTGA 500
QY 481 TGCTGGCAGCACATTTCTTGAATCTCCAGGCTGCAGAAACATTGGCTAATATGACAG 540
Db 501 -----ATATGGACAG 510
QY 541 AGACATGGAATAATTAAGAAAGCTGTGGGTACTCAAGAACTCTTGTACCTTACC 600
Db 511 AGACATGGAATAATTAAGAAAGCTGTGGGTACTCAAGAACTCTTGTACCTTACC 570
QY 601 AGTGAACCTCAGACATACAGGAACCTTATTAACGGAGGAGGAGGCGGCTGGG 660
Db 571 AGTGAACCTCAGACATACAGGAACCTTATTAACGGAGGAGGAGGCGGCTGGG 630
QY 661 AGCTACTCAGATGAGCATGACGCGGCTTCACTCCCTGGTGGAAAAAATAGAT 720
Db 631 AGCTACTCAGATGAGCATGACGCGGCTTCACTCCCTGGTGGAAAAAATAGAT 690
QY 721 CCTCCAGTCAATATTAACCAAGTCAATGAGCTTGTGGTATATCTCATCTCCA 780
Db 691 CCTCCAGTCAATATTAACCAAGTCAATGAGCTTGTGGTATATCTCATCTCCA 750
QY 781 AATTACCATATAGATACCAAAAGAAAAAATATATCTATAGAGATTACTATGACTA 840
Db 751 AATTACCATATAGATACCAAAAGAAAAAATATATCTATAGAGATTACTATGACTA 810
QY 841 CTATACGAGTTTATATTAATTAACATTTCACTAAGAAAGGCAAAAGCTTATGACGG 900
Db 811 CTATACGAGTTTATATTAATTAACATTTCACTAAGAAAGGCAAAAGCTTATGACGG 870

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QY 901 GCTCAGAGCGGTTGAAATTGAACTCTAACACCACTCCAGCTACTGTAGTGGCT 960
DB 871 GCTCAGAGCGGTTGAAATTGAACTCTAACACCACTCCAGCTACTGTAGTGGCT 930
QY 961 GAAATATATCAGCCCATGTTAGACAGAGAGAGTCAAGAGAGAGAGATGTGGAA 1020
DB 931 GAAATATATCAGCCCATGTTAGACAGAGAGAGTCAAGAGAGAGAGATGTGGAA 990
QY 1021 ATTCATGACTTGTGAAATTGGCATTCGCAATGTGAATTTAAAGCTCCAGAA 1080
DB 991 ATTCATGACTTGTGAAATTGGCATTCGCAATGTGAATTTAAAGCTCCAGAA 1050
QY 1081 CAGATGACTGCTGTTTAAAGATCTTAAATGTTTGTATTTTCTTAAAGCAA 1140
DB 1051 CAGATGACTGCTGTTTAAAGATCTTAAATGTTTGTATTTCTTAAAGCAA 1110
QY 1141 TATTCACGTTCACCTGGGAGCTCTTGTATTCATCTTTTATTCCTTATATTC 1200
DB 1111 TATTCACGTTCACCTGGGAGCTCTTGTATTCATCTTTTATTCCTTATATTC 1170
QY 1201 ATTTGTAACCTATATTTGACGACATCTCCCGGAAATTTGAATGTAAGATGAGGCA 1260
DB 1171 ATTTGTAACCTATATTTGACGACATCTCCCGGAAATTTGAATGTAAGATGAGGCA 1230
QY 1261 GAGATTAAGTGTCTATGAAA 1282
DB 1231 GAGATTAAGTGTCTATGAAA 1252

RESULT 5
ABK50076
ID ABK50076 standard; DNA; 2271 BP.
AC
XX ABK50076;
XX
XX 15-JUL-2002 (first entry)
XX
XX DNA encoding human IL-TIF/IL-22 binding protein #1.
XX
XX Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
XX IL-TIF/IL-22 antagonist; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 110..805
XX FT /product="Human IL-TIF/IL-22 binding protein #1"
XX /note="This sequence can optionally start at
XX position 113"
XX
XX WO200224912-A2.
XX
XX 28-MAR-2002.
XX
XX 21-SEP-2001; 2001WO-US29576.
XX
XX 22-SEP-2000; 2000US-234583P.
XX 03-NOV-2000; 2000US-245495P.
XX 31-JUL-2001; 2001US-0919162.
XX
XX (LUDWIG-) LUDWIG INST CANCER RES.
XX
XX Renauld J, Dumoutier L;
XX
XX WPI; 2002-383190/41.
XX
XX P-PSDB; AAU80000.
XX
XX polynucleotide and polypeptide of soluble protein which binds to
XX interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
XX cell
XX
XX Claim 1; Page 38-39; 42pp; English.
```

```
XX
CC The present invention relates to a new polynucleotide that encodes a
CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
CC to as IL-22BP), where the complementary sequence of the invention
CC hybridises under stringent conditions to a nucleotide sequence of 2271
CC or 2366 base pairs, as given in the specification. The molecules of the
CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
CC in vitro, and for obtaining an antibody molecule specific for the soluble
CC binding protein of the invention. From a population or panel of antibody
CC molecules of diverse binding specificity. The soluble protein is further
CC useful in manufacture of a medicament for treating an IL-22 mediated
CC disease and for assaying an agent, preferably an antibody or a peptide
CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
CC of the soluble protein to IL-TIF/IL-22, where the agent identified is
CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
CC disorder. The antibody is useful for determining presence of the soluble
CC protein, where the antibody is detectably labelled. The present nucleic
CC acid sequence encodes the human IL-TIF/IL-22 binding protein #1 of the
CC invention.
CC
SQ Sequence 2271 BP; 709 A; 400 C; 444 G; 718 T; 0 other:
XX
XX
XX Query Match 69.0%; Score 910; DB 24; Length 2271;
XX Best Local Similarity 91.0%; Pred. No. 1; 1e-178;
XX Matches 1019; Conservative 0; Mismatches 5; Indels 96; Gaps 1;
QY 170 CTGTTCTCTTTGGTCCGAGCTGGTTAAAGAACTGGTGGCTGACAGTACAC 229
DB 42 CAGTTTCCCTTTGGTCCGAGCTGGTTAAAGAACTGGTGGCTGACAGTACAC 101
QY 230 TTGCACCATGATGCTTAACATTTCTTCTAGGCTTCTCCTCAGTTTCTTCTTCTG 289
DB 102 TTGCACCATGATGCTTAACATTTCTTCTAGGCTTCTCCTCAGTTTCTTCTTCTG 161
QY 290 GTGTAGCAGAACTCAGTCAACGATGATCTCTGAAGCTTCAAGAGGTACATTTCACT 349
DB 162 GTGTAGCAGAACTCAGTCAACGATGATCTCTGAAGCTTCAAGAGGTACATTTCACT 221
QY 350 CCCGAATTTTCAACAACTTTTGAAGTGGCAGCTGGGAGGACACTTATGCAACAGCA 409
DB 222 CCCGAATTTTCAACAACTTTTGAAGTGGCAGCTGGGAGGACACTTATGCAACAGCA 281
QY 410 GTGTATTTTGTGCAAGTACAAATCATGTTCTCATGACATGAAAGCTCTCACCAGA 469
DB 282 GTGTATTTTGTGCAAGTACAAATCATGTTCTCATGACATGAAAGCTCTCACCAGA 306
QY 470 AGCCAAGTGGATGCTGGCAGACATTTCTTGTACTTCCAGAGCTGCAACATTTGGCTA 529
DB 307 ----- 306
QY 530 AATATGACAGAGACAAATGAAATAAAGAACTGTTGGGTACTCAAGAACTCTCTT 589
DB 307 AATATGACAGAGACAAATGAAATAAAGAACTGTTGGGTACTCAAGAACTCTCTT 365
QY 590 GTGACCTTACAGAGTGAACCTCAGACATACAGAACTTATTAAGGAGGTGAGGGCGG 649
DB 366 GTGACCTTACAGAGTGAACCTCAGACATACAGAACTTATTAAGGAGGTGAGGGCGG 425
QY 650 CCTGGGCTGGAGCTACTAGATGAGATGAGCATGACGGCGGCTCCTCCCTGGTGGGAAA 709
DB 426 CCTGGGCTGGAGCTACTAGATGAGATGAGCATGACGGCGGCTCCTCCCTGGTGGGAAA 485
QY 710 CAAATATAGATCCTCAGTCAATGATATTAACCAAGTCAATGAGCTCTTGTGTATATTC 769
DB 486 CAAATATAGATCCTCAGTCAATGATATTAACCAAGTCAATGAGCTCTTGTGTATATTC 545
QY 770 TCCATGCTCCAAATTTTACATATATATACCAAAAGGAAAAATGATCTATAGAGATT 829
DB 546 TCCATGCTCCAAATTTTACATATATATACCAAAAGGAAAAATGATCTATAGAGATT 605
QY 830 ACTATGACTACTATACCGAGTTTATATATTAATTAACATTCACAGAAAGGACCAAGG 889
```


Accession	Gene	Protein	Location/Qualifiers
Dn	606	ACTA1GAACTACTATACGAGGTTTATTATTAATTAACAAATTCCTAAGAAAGGACAAAAG	1189
Qy	890	TTTATGAAGGGGCTCACAAGCGGTTGAAATTTGAAGCTCTAACCACACTCCAGCTACT	949
Dn	666	TTTATGAAGGGGCTCACAAGCGGTTGAAATTTGAAGCTCTAACCACACTCCAGCTACT	725
Qy	950	GTGATGTCGGAATTAATATGACCCAGCTTAGACAGAAGAGTACAGAACTGAAGAGA	1009
Dn	726	GTGATGTCGGAATTAATATGACCCAGCTTAGACAGAAGAGTACAGAACTGAAGAGA	785
Qy	1010	GATGTCGGAATTAATATGACCCAGCTTAGACAGAAGAGTACAGAACTGAAGAGA	1066
Dn	786	GATGTCGGAATTAATATGACCCAGCTTAGACAGAAGAGTACAGAACTGAAGAGA	845
Qy	1070	CTCCCTGAGAACAGAGTACTCGTTTGAAGATCTTATTTAAATTTGTTTGTATTT	1122
Dn	846	CTCCCTGAGAACAGAGTACTCGTTTGAAGATCTTATTTAAATTTGTTTGTATTT	905
Qy	1130	TCTTAAGCAATATTCACCTGTAAACCTCTGGGACCTCTTGTATTCATCTTTATTC	1189
Dn	906	TCTTAAGCAATATTCACCTGTAAACCTCTGGGACCTCTTGTATTCATCTTTATTC	965
Qy	1190	CTTATATTTCAATTTGAACCTATATTTGAAGCACTTCCCGGAAATTTGAATGTA	1249
Dn	966	CTTATATTTCAATTTGAACCTATATTTGAAGCACTTCCCGGAAATTTGAATGTA	1025
Qy	1250	AAGATGAGCAGAGATTAAGTGTCTCATGAAAAA 1289	
Dn	1026	AAGATGAGCAGAGATTAAGTGTCTCATGAAAAA 1065	
RESULT 6			
AAD09745			
ID	AAD09745	standard; cDNA; 2149 BP.	
AC	AAD09745;		
XX			
DT	10-SEP-2001	(first entry)	
XX			
DE	Human ZCYTO18 soluble receptor antagonist cDNA, zcytor16.		
XX			
KM	Human; cytosolic; cytokine; ZCYTO18 protein; genetic abnormality;		
KW	cancer; inflammation; gene therapy; zcytor16; ss.		
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
CDS	1..696		
FT	1..696		
XX			
PN	WO200146422-A1.		
XX			
PD	28-JUN-2001.		
XX			
PF	22-DEC-2000; 2000WO-US35308.		
XX			
PR	23-DEC-1999; 99US-0471767.		
XX			
PR	01-DEC-2000; 2000US-0250841.		
XX			
PA	(ZYMO) ZYMOGENETICS INC.		
XX			
PI	Presnell SR, Kindsvogel W;		
XX			
DR	WPI; 2001-408648/43.		
XX			
DR	P-PSDB; AAE05048.		
XX			
XX			
PT	Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer		
XX			
PS	Example 13A; Page 156-158; 167pp; English.		
XX			
CC	The patent discloses novel human cytokine, ZCYTO18 protein and its		

Query Match	63.1%	Score 831.6	DB 22	Length 2149
Best Local Similarity	90.4%	Pred. 1.8e-162		
Matches 951	Conservative 0	Mismatches 4	Indels 97	Gaps 2
238 ATGATGCGCTAAACATTGCTTTCTAGGCTTCCTCATCTAGTTCTTCTCTTACTGTGTAGCA				297
1 ATATGCGCTAAACATTGCTTTCTAGGCTTCCTCATCTAGTTCTTCTCTTACTGTGTAGCA				60
298 GGAACACAGTCAACAGCATGAGTCTCGAAGCCCTCAGAGGGTCAATTTGACGCCGAAT				357
61 GGAACACAGTCAACAGCATGAGTCTCGAAGCCCTCAGAGGGTCAATTTGACGCCGAAT				120
358 TTTTCACAACTTTTGCATGGCAGCCTGGGAGGCACTTACTGGCAACAGCATGTCTAT				417
121 TTTTCACAACTTTTGCATGGCAGCCTGGGAGGCACTTACTGGCAACAGCATGTCTAT				180
418 TTTTGCATACAAATTCATGTTCATCAGCATGAAAAGCTCTCACCAGAAGCCAAAGT				477
181 TTTTGCATACAAATTCATGTTCATCAGCATGAAAAGCTCTCACCAGAAGCCAAAGT				197
478 GGAATGCTGGCAGCAGCATTTCTGTAACTTCCAGGCTGAGAAACAATTTGGCTAATATGA				537
198 -----AATATGA				204
538 CAGAGCAATGCAAAAATAAAGACAGTGTGGGTACTCAGAACCTCTGTGACCTT				597
205 CAGAGCAATGCAAAAATAAAGACAGTGTGGGTACTCAGAACCTCTGTGACCTT				264
598 ACCAGTGAACCTCAGACATACAGAACCTTATTACGGAGGGGTAGGGCGGCTCGGCT				657
265 ACCAGTGAACCTCAGACATACAGAACCTTATTACGGAGGGGTAGGGCGGCTCGGCT				324
658 GGGAGCTACTCAGATGGAGCATGAGCGCGGGGTCACTCCCTGGTGGGAAACAAAATA				717
325 GGGAGCTACTCAGATGGAGCATGAGCGCGGGGTCACTCCCTGGTGGGAAACAAAATA				384
718 GATCTCGAGTCATGAATATAACCCAACTCAATGGCTTTGTGGTAAATCTCATGCT				777
385 GATCTCGAGTCATGAATATAACCCAACTCAATGGCTTTGTGGTAAATCTCATGCT				444
778 CCAATTTACATATAGTACCCAAAAGAAAAATGTATCTATAGAAAGATTACTATGAA				837
445 CCAATTTACATATAGTACCCAAAAGAAAAATGTATCTATAGAAAGATTACTATGAA				504
838 CTACATATCCAGTCTTTATATTAATTAACAATTCACCTAGAAAAAGAGCAAAAGTTATGAA				897
505 CTACATATCCAGTCTTTATATTAATTAACAATTCACCTAGAAAAAGAGCAAAAGTTATGAA				564
898 GGGGCTCAGAGAGCGGTGAATTTGAAGCTTAAACCCACTCCAGCTACTGTGTAGTG				957
565 GGGGCTCAGAGAGCGGTGAATTTGAAGCTTAAACCCACTCCAGCTACTGTGTAGTG				624
958 GCTGAATATATTCAGCCCATGTTAGACAGAAAGAGTCAAGAACTGAAAGAGATGTGTG				1017
625 GCTGAATATATTCAGCCCATGTTAGACAGAAAGAGTCAAGAACTGAAAGAGATGTGTG				684
1018 GAAATTCATATCACTTTGGGAATTTGGCATTCAGCAATGTGTAATTTTAAAGCTCCCTGA				1077
685 GAAATTCATATCACTTTGGGAATTTGGCATTCAGCAATGTGTAATTTTAAAGCTCCCTGA				744
1078 GAAACGATGACATGCTGTTTGAAGATCTTATTTAAATTTGTTTGTATTTCTTAAAG				1137

Db 745 GAAAGGATGACTGCTGTTGAAGGATCTTATTAAGTTGTTGTTGTTTAAAG 804
 1138 CAATATTCACGTTACACCTGGGAGCTTCTTTGTTATCCATCTTTTATCCCTTAAAT 1197
 Db 805 CAATATTCACGTTACACCTGGGAGCTTCTTTGTTATCCATCTTTTATCCCTTAAAT 864
 QY 1198 TTCAATTTGTAACATATATTTGTAAGACATTCCTCCCGGAAATTTGAATGTAAGATGAG 1257
 Db 865 TTCAATTT-TAAACTATATTTGTAAGACATTCCTCCCGGAAATTTGAATGTAAGATGAG 923
 QY 1258 GCAGAGATTAAGTGTCTATGAAAAA 1289
 Db 924 GCAGAGATTAAGTGTCTATGAAAAATTCAGAA 955
 RESULT 7
 AAF83735
 ID AAF83735 standard; cDNA, 2149 BP.
 AAF83735;
 DT 23-JUL-2001 (first entry)
 XX Human cytokine receptor, zcytor16 encoding cDNA.
 DE Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
 KW antineumatic; antiarthritic; antialsthatic; antiatherosclerotic;
 KW immunosuppressive; chromosome 6q24.1-25.2; human; ss.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 1.696
 FT CDS /tag=2
 FT /product="zcytor16"
 XX MO200140467-A1.
 PM 07-JUN-2001.
 XX 01-DEC-2000; 2000WO-US32703.
 XX 03-DEC-1999; 99US-0169049.
 PR 13-SEP-2000; 2000US-0232219.
 PR 31-OCT-2000; 2000US-0244610.
 XX (ZYMO) ZYMOGENETICS INC.
 PR Presnell SR, Xu W, Kindsvogel W, Chen Z;
 DR WPL: 2001-356158/37.
 DR P-PSDB: AAB62657.
 XX New soluble cytokine receptor polypeptides and polynucleotides, useful
 PT for diagnosing and treating cancer and inflammatory conditions - useful
 XX Claim 10; Page 186-188; 210pp; English.
 PS The invention relates to a human cytokine receptor polypeptide,
 CC designated zcytor16. The zcytor16 polypeptide can be expressed by
 CC standard recombinant methodology and can bind to IL-TIF (undefined). The
 CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
 CC or differentiation of hematopoietic cell(s) (progenitors); reducing
 CC IL-TIF induced or IL-9 induced inflammation; and suppressing an
 CC inflammatory response in a mammal with inflammation. Heteromeric/
 CC multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be
 CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
 CC can also be used to detect IL-TIF levels which is indicative of
 CC pathological conditions including inflammatory states (e.g. rheumatoid
 CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
 CC polypeptides themselves are useful for the treatment of inflammation,
 CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel

CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune
 CC diseases. The antibodies and zcytor16 polynucleotides are also useful
 CC for detecting cancer. The present sequence represents a cDNA encoding
 CC the human zcytor16 protein.
 XX

SQ Sequence 2149 BP; 685 A; 381 C; 421 G; 662 T; 0 other;

Query Match 63.1%; Score 831.6; DB 22; Length 2149;

Best Local Similarity 90.4%; Pred. No. 1.8e-162;

Matches 951; Conservative 0; Mismatches 4; Indels 97; Gaps 2;

QY 238 ATGATGCTTAACCAATTCCTTCTAGGCTTCTCATCAGTTTCTTCTTACGTTAGCA 297
 Db 1 ATGATGCTTAACCAATTCCTTCTAGGCTTCTCATCAGTTTCTTCTTACGTTAGCA 60
 QY 298 GGAACCTAGTCACGATGATGATCTCTGAAAGCTCAGAGGATCAATTCAGTCCGGAAT 357
 Db 61 GGAACCTAGTCACGATGATGATCTCTGAAAGCTCAGAGGATCAATTCAGTCCGGAAT 120
 QY 358 TTTCACAAATTTTGCATATGACGCTGGAGGCGACTTACTGGCAGACAGAGTCTAT 417
 Db 121 TTTCACAAATTTTGCATATGACGCTGGAGGCGACTTACTGGCAGACAGAGTCTAT 180
 QY 418 TTTGTGAGTACAAATTCATGTTCTCATGCAGATGAAAAGCTCTCACCAGAGCAAGT 477
 Db 181 TTTGTGAGTACAAATTCATGTTCTCATGCAGATGAAAAGCTCTCACCAGAGCAAGT 197
 QY 478 GGATGCTGGAGCAGCATTTCTTGTAACTTCCAGGCTGCAAGAACATTTGGCTAATATGCA 537
 Db 198 -----AATGGA 204
 QY 538 CAGAGCAATGAAAAAATTAAGAAAGACTGTTGGGTACTCAGAACTCTCTTGTGACCTT 597
 Db 205 CAGAGCAATGAAAAAATTAAGAAAGACTGTTGGGTACTCAGAACTCTCTTGTGACCTT 264
 QY 598 ACCAGTGAACCTCAGACATACAGAACCTTATACGGAGGCTGAGGCGCTCGGCT 657
 Db 265 ACCAGTGAACCTCAGACATACAGAACCTTATACGGAGGCTGAGGCGCTCGGCT 324
 QY 658 GGGAGCTACCTCAGATGAGAGCATGACGCGCGGTTCACCTCCCTGGTGGAAACAAAATA 717
 Db 325 GGGAGCTACCTCAGATGAGAGCATGACGCGCGGTTCACCTCCCTGGTGGAAACAAAATA 384
 QY 718 GATCCTCAGTCATGATATTAACCAAGTCAATGGCTCTTTGTTGTAATTCCTCATGCT 777
 Db 385 GATCCTCAGTCATGATATTAACCAAGTCAATGGCTCTTTGTTGTAATTCCTCATGCT 444
 QY 778 CCAATTTACCTATATAGATACCAAAAGAAAAAATGTATCTATAGAAATTCATATGAA 837
 Db 445 CCAATTTACCTATATAGATACCAAAAGAAAAAATGTATCTATAGAAATTCATATGAA 504
 QY 838 CTACTATACCGAGTTTATATTAATTAACAATTCATAGAAAGAGCAAAAGGTTTATGAA 897
 Db 505 CTACTATACCGAGTTTATATTAATTAACAATTCATAGAAAGAGCAAAAGGTTTATGAA 564
 QY 898 GGGGCTCAGAGCGGCTTGAATTTGAAGCTCTACACCAACCTCCAGCTACTGTGATG 957
 Db 565 GGGGCTCAGAGCGGCTTGAATTTGAAGCTCTACACCAACCTCCAGCTACTGTGATG 624
 QY 958 GCTGAATTTATCAGCCCATGTTAGACAGAGAGTCAAGAGAGATGATG 1017
 Db 625 GCTGAATTTATCAGCCCATGTTAGACAGAGAGTCAAGAGAGATGATG 864
 QY 1018 GAAATTCATGACTTGTGAAATTTGGCAATTCAGCAATGTGAAATTTCTAAGCTCCCTGA 1077
 Db 685 GAAATTCATGACTTGTGAAATTTGGCAATTCAGCAATGTGAAATTTCTAAGCTCCCTGA 744
 QY 1078 GAACAGAGATGACTGCTTGAAGATCTTATTAATTTGTTGTTATTTCTTAAAG 1137
 Db 745 GAACAGAGATGACTGCTTGAAGATCTTATTAATTTGTTGTTATTTCTTAAAG 804
 QY 1138 CAATATTCACGTTACACCTGGGAGCTTCTTGTATCCATTTCTTAAATTTCTTAAAT 1197

Db 805 CAATATTCACCTGTACACCTTGGGACCTCTTGTATTACATCTCTTATAT 864
 QY 1198 TTCAATTTGAACATAATTTAGACATTCCTCCCGAAATTTGAATGTAAGTGG 1257
 Db 865 TTCAATTT-TTAACTATATTTAAGACACTTCCCGGAAATTTGAATGTAAGTGG 923
 QY 1258 GCAGAGATTAAGTGTCTATGAAAAA 1289
 Db 924 GCAGAGATTAAGTGTCTATGAAATTCAGAA 955
 RESULT 8
 ID AAL46001 standard; cdna; 810 BP.
 AC AAL46001;
 DT 08-AUG-2002 (first entry)
 XX Human cytokine receptor variant 3 coding sequence.
 Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
 rheumatoid arthritis; multiple sclerosis; Crohn's disease;
 ulcerative colitis; transplant rejection; abortion; antipsoriatic;
 immunosuppressive; antineumatic; antiarthritic; neuroprotective;
 antiinflammatory; antilucer; cyostatic; dermatological;
 chromosome 6q24.1-25.2; receptor; gene; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 12..803
 FT /tag= a
 FT /product= "cytokine receptor variant 3"
 EP1191035-A2.
 27-MAR-2002.
 24-AUG-2001; 2001EP-0250307.
 PF 25-SEP-2000; 2000DE-1048626.
 PR 17-NOV-2000; 2000DE-1058907.
 PR 19-DEC-2000; 2000DE-1064906.
 XX (SCHD) SCHERING AG.
 PA Weiss B, Sabat R, Assadullah K, Toshi L;
 XX WPI: 2002-332210/37.
 DR P-PSDB; AAO17382.
 XX New nucleic acid encoding soluble cytokine receptor, useful for
 PT diagnosis and treatment of e.g. immune disease, also related protein
 PR and antibodies
 XX
 PS Claim 1; Page 14-15; 21pp; German.
 CC The present invention provides the protein and coding sequences of 3
 CC variants of a human cytokine receptor. The sequences can be used in the
 CC diagnosis, prevention and treatment of immune diseases, including
 CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
 CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
 CC transplant rejection and in reproductive medicine, e.g. for diagnosing
 CC abnormal immune reactions which cause abortions. The present sequence is
 CC the coding sequence of variant 3 of the invention.
 SO Sequence 810 BP; 253 A; 172 C; 184 G; 201 T; 0 other;

Query Match 61.1%; Score 805.2; DB 24; Length 810;
 Best Local Similarity 99.6%; Pred. No. 4.1e-157;
 Matches 807; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 227 CACTTGCAACCATGATGCTTAACATTTGCTTGTAGCCTTCCTCATGATTTCTCTTA 286
 Db 1 CACTTGCAACCATGATGCTTAACATTTGCTTGTAGCCTTCCTCATGATTTCTCTTA 60
 QY 287 CTGGTGTAGAGAGAACTCACTCAACGCATGAGTGTCTGAAAGCCCTCAGAGGTTACAAATTC 346
 Db 61 CTGGTGTAGAGAGAACTCACTCAACGCATGAGTGTCTGAAAGCCCTCAGAGGTTACAAATTC 120
 QY 347 AGTCCGGAATTTTTCACACATTTTGCATGAGCCCTGGAGGAGCACTTACTGGCAACA 406
 Db 121 AGTCCGGAATTTTTCACACATTTTGCATGAGCCGAGGAGGAGCACTTACTGGCAACA 180
 QY 407 GCAGTGTCTATTTTGTGCAATGAAAAATCAATGTTCTCATGAGCATGAAAAAGCTCTACC 466
 Db 181 GCAGTGTCTATTTTGTGCAATGAAAAATCAATGTTCTCATGAGCATGAAAAAGCTCTACC 240
 QY 467 AGAAGCAAGTGTGATGCTGAGCAGACATTTCTGTACTTCCCGGCTGCAGAACATTTGG 526
 Db 241 AGAAGCAAGTGTGATGCTGAGCAGACATTTCTGTACTTCCCGGCTGCAGAACATTTGG 300
 QY 527 CTAAATATGACAGACAGACAAATGAAAAATTAAGAGACTGTTGGGTTACTCAAGACTCT 586
 Db 301 CTAAATATGACAGACAGACAAATGAAAAATTAAGAGACTGTTGGGTTACTCAAGACTCT 360
 QY 587 CTGTGACCTTACAGTGAACCTCAGACATACAGAACCTTATTACGGAGGTTGAGGG 646
 Db 361 CTGTGACCTTACAGTGAACCTCAGACATACAGAACCTTATTACGGAGGTTGAGGG 420
 QY 647 CGGCTCGGCTGGAGCTACTCAGAAATGAGCATGAGCGCGGTTCACTCCCTGGTGGG 706
 Db 421 CGGCTCGGCTGGAGCTACTCAGAAATGAGCATGAGCGCGGTTCACTCCCTGGTGGG 480
 QY 707 AAACAAAAATAGATCTCTCCAGTCTATCAATTAACCAAGTCAATGCTCTTGTGTGTA 766
 Db 481 AAACAAAAATAGATCTCTCCAGTCTATCAATTAACCAAGTCAATGCTCTTGTGTGTA 540
 QY 767 TTCTCCATGCTCAAAATTTACCATATAGATACCAAAAGAAAAATGTTCTATAGAA 826
 Db 541 TTCTCCATGCTCAAAATTTACCATATAGATACCAAAAGAAAAATGTTCTATAGAA 600
 QY 827 ATTACTAGACTACTATACCGAGTTTATATTAATTAACATTCCTAGAAAGAGCAAA 886
 Db 601 ATTACTAGACTACTATACCGAGTTTATATTAATTAACATTCCTAGAAAGAGCAAA 660
 QY 887 AGGTTATGAAGGGGCTCAGAGCGGTTGAATTAAGCTTACACCACTCCAGCT 946
 Db 661 AGGTTATGAAGGGGCTCAGAGCGGTTGAATTAAGCTTACACCACTCCAGCT 720
 QY 947 ACTGTGTAGTGCTGAATATATATCAAGCCCATGTAGACAGAAAGTCAAGAGGAAG 1006
 Db 721 ACTGTGTAGTGCTGAATATATATCAAGCCCATGTAGACAGAAAGTCAAGAGGAAG 780
 QY 1007 AGAGATGTGTGAAATTCATGACTTGTGG 1036
 Db 781 AGAGATGTGTGAAATTCATGACTTGTGG 810

RESULT 9
 AAD27816
 ID AAD27816 standard; DNA; 792 BP.
 AC AAD27816;
 DT 18-Apr-2002 (first entry)
 XX Human cytokine receptor gene, sbg456548CytoKa #3.
 KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
 KW autoimmune disorder; hematopoietic disorder; inflammation; arthritis;
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarthritic;
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
 KW depression; cardiovascular disease; myocardial infarction; renal failure;

KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hyperplasia; renal disease; hypoglycaemia; gastrointestinal disease;
KW neoplastic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
KW haemostatic; vitreous; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
KW allergy; cytokine receptor; gene; ds.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH 1..696 /tag= a
FT CDS /product= "Human cytokine receptor"
FM
FM
WO200198342-A1.
PD 27-DEC-2001.
XX 22-JUN-2001; 2001WO-US19929.
PF 22-JUN-2000; 2000US-213156P.
PR 22-JUN-2000; 2000US-213161P.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX (GLAXO) GLAXO GROUP LTD.
XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX WPI: 2002-139783/18.
XX P-PSDB: AAE17320.
XX
XX Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or
PT disease including diabetes, cancer, hypertension and growth
PT abnormalities
XX
XX Claim 2; Page 98; 138pp; English.
XX
XX The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesterol ester storage disease,
CC inflammation, congenital muscular dystrophy, junctional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, shg44245PROA-associated disorders,
CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft versus host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including paraneuronal palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease,
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,

CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
XX The present sequence is human cytokine receptor gene.
SQ Sequence 696 BP; 224 A; 140 C; 157 G; 175 T; 0 other;
Query Match 44.8%; Score 590; DB 24; Length 696;
Best Local Similarity 87.9%; Pred. No. 1.2e-112;
Matches 696; Conservative 0; Mismatches 0; Indels 96; Gaps 1;
QY 238 ATGATGCTTAACATTCGTTCTTAGGCTTCCTCATCAGTTCCTTCTTACTGTTAGCA 297
DB 1 ATGATGCTTAACATTCGTTCTTAGGCTTCCTCATCAGTTCCTTCTTACTGTTAGCA 60
QY 298 GGAAGCTCAGTACAGCATGAGCTCTGTAAGCCTCAGAGGGTACATTCAGTCCGGAAT 357
DB 61 GGAAGCTCAGTACAGCATGAGCTCTGTAAGCCTCAGAGGGTACATTCAGTCCGGAAT 120
QY 358 TTTCACACATTTTGCATGCGAGCTGGAGGGGACCTTACTGCGACAGCAGTGTCTAT 417
DB 121 TTTCACACATTTTGCATGCGAGCTGGAGGGGACCTTACTGCGACAGCAGTGTCTAT 180
QY 418 TTTCGACGTCACAAATATGCTTCTCATGACGATGAAAAGCTTCACCAAGCCAGCT 477
DB 181 TTTCGACGTCACAAAT----- 197
QY 478 GGATGCTGGGACGACATTTCTTGTACTTCCAGGCTGAGACACATGGCTAAATATGA 537
DB 198 -----ATATGA 204
QY 538 CAGAGACATGGAATAATTAAGAGACTGTTGGGTACTCAAGACCTCTGTGACCT 597
DB 205 CAGAGACATGGAATAATTAAGAGACTGTTGGGTACTCAAGACCTCTGTGACCT 264
QY 598 ACCAGTGAACCTCAGACATACAGAACCTTATTAAGGAGGTGAGGGCGGCTGCT 657
DB 265 ACCAGTGAACCTCAGACATACAGAACCTTATTAAGGAGGTGAGGGCGGCTGCT 324
QY 658 GGGAGTACTCAGAAATGAGATGAGATGAGCGCGGTTCACTCCCTGGTGGAAACAAAATA 717
DB 325 GGGAGTACTCAGAAATGAGATGAGATGAGCGCGGTTCACTCCCTGGTGGAAACAAAATA 384
QY 718 GATCCTCAGTCAATGAATTAACCAAGTCAATGCTTGTGTGTAATTCATGCT 777
DB 385 GATCCTCAGTCAATGAATTAACCAAGTCAATGCTTGTGTGTAATTCATGCT 444
QY 778 CCAATTTACCATATGATTAACCAAGGAAAAAATGATATATGAAGATTATGA 837
DB 445 CCAATTTACCATATGATTAACCAAGGAAAAAATGATATATGAAGATTATGA 504
QY 838 CTACTATACGAGTTTATTAATTAACCAATTCACATGAGAAAGGACCAAAAGTTATGA 897
DB 505 CTACTATACGAGTTTATTAATTAACCAATTCACATGAGAAAGGACCAAAAGTTATGA 564
QY 898 GGGGCTCAGACAGCGGTTGAATTAACCTTAACCAACTCCAGTACTGTTAGTG 957
DB 565 GGGGCTCAGACAGCGGTTGAATTAACCTTAACCAACTCCAGTACTGTTAGTG 624
QY 958 GCTGAATATATATCAAGCCCATGTTAGACAGAAAGAACTCAGAGAAGTGAAGAGATGTGTG 1017
DB 625 GCTGAATATATATCAAGCCCATGTTAGACAGAAAGAACTCAGAGAAGTGAAGAGATGTGTG 684
QY 1018 GAAATTCATGA 1029
DB 685 GAAATTCATGA 696
RESULT 11
AAD06414
ID AAD06414 standard; cDNA; 696 BP.
XX AC AAD06414;
XX

DT 10-AUG-2001 (first entry)
 XX Human DNAX cytokine receptor subunit 4.2 (DCRS4.2) cDNA.
 DE Human DNAX cytokine receptor subunit 4.2; DCRS4.2;
 KW Human; immunomodulator; DNAX cytokine receptor subunit 4.2; DCRS4.2;
 KM therapy; immunological disorder; drug screening; cell development;
 KW chromosome 6q24.1-25.2; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..696
 FT /tag= a
 FT /product= "Human DNAX cytokine receptor subunit 4.2
 FT (DCRS4.2)"
 FT 1..63
 FT sig_peptide /tag= b
 FT 64..693
 FT mat_peptide /tag= c
 FT /product= "Human mature DNAX cytokine receptor
 subunit 4.2 (DCRS4.2)"
 CC WO200136467-A2.
 PN 25-MAY-2001.
 XX 16-NOV-2000; 2000WO-US31363.
 PF 18-NOV-1999; 99US-0443060.
 PR 13-DEC-1999; 99US-0170320.
 XX (SCHE) SCHERING CORP.
 PA Gorman DM;
 PI WPI: 2001-343800/36.
 DR P-PSDB: AAE02460.
 XX
 PT New mammalian receptor proteins related to cytokine receptors, useful
 PT for regulating cell development and for diagnosis and treatment of
 PT immunological disorders
 PS
 XX Claim 16; Page 22; 124pp; English.
 CC The present sequence is human DNAX cytokine receptor subunit 4.2
 CC (DCRS4.2) cDNA. DCRS4 gene is located on chromosome 6q24.1-25.2.
 CC Cytokine receptors, fragments and antibodies are useful for treating
 CC immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
 CC useful in drug screening to identify compounds having binding affinity
 CC to the receptor subunit. Modulators of DCRS are useful for modulating
 CC the physiology or development of a cell or tissue culture cells. A
 CC purified DCRS is useful as a reagent to detect antibodies generated in
 CC response to the presence of elevated levels of expression, or
 CC immunological disorders which lead to production of antibody to the
 CC endogenous receptor. Cytokine receptor sequences are useful as probes
 CC for detecting levels of the cytokine receptor in patients suspected of
 CC having an immunological disorder. Antibodies have therapeutic value, are
 CC useful as potent antagonist, in detecting or quantifying ligands, for
 CC isolating DCRS proteins and peptides, to screen expression libraries for
 CC particular expression products, to raise anti-idiotypic antibodies and
 CC for detecting or diagnosing various immunological conditions related to
 CC expression of the protein or cells which express the protein.
 XX
 XX Sequence 696 BP; 224 A; 141 C; 157 G; 174 T; 0 other;
 Query Match 44.6%; Score 588.4; DB 22; Length 696;
 Best Local Similarity 87.8%; Pred. No. 2.5e-112;
 Matches 695; Conservative 0; Mismatches 1; Indels 96; Gaps 1;
 OY 238 ATGATGCTTAACATGCTTCTAGGCTTCATCAGTGTCTTCTTCTACTGTAGCA 297
 DB 1 ATGATGCTTAACATGCTTCTAGGCTTCATCAGTGTCTTCTTCTACTGTAGCA 60

OY 298 GGAACCTAGCTCAACGCAATGAGTCTCTGAGGCTCAGAGGTACAAATTTTCAGTCCGAAT 357
 DB 61 GGAACCTAGCTCAACGCAATGAGTCTCTGAGGCTCAGAGGTACAAATTTTCAGTCCGAAT 120
 OY 358 TTTCACACATTTTTCAGATGGCAGCTGGAGGGGCACTTACTGGCAACAGAGTGTAT 417
 DB 121 TTTCACACATTTTTCAGATGGCAGCTGGAGGGGCACTTACTGGCAACAGAGTGTAT 180
 OY 418 TTGTGCGATCAAAATTCATGTTCTCATGCAGCATGAAAACCTCTCACCAGACCAAGT 477
 DB 181 TTGTGCGATCAAAATTCATGTTCTCATGCAGCATGAAAACCTCTCACCAGACCAAGT 197
 OY 478 GGATGCTGCGAGCAGATTTTCTGATCTCCAGGCTCAGACATTTGGTAAATATGA 537
 DB 198 -----AATGGA 204
 OY 538 CAGAGCAATGGAAAAATTAAGAGACTGTTGGGTTACTCAAGACTCTGTTGACCTT 597
 DB 205 CAGAGCAATGGAAAAATTAAGAGACTGTTGGGTTACTCAAGACTCTGTTGACCTT 264
 OY 598 ACCAGTAAACCTCAGACATCAGAGAACCTTATTCGGAGAGGTGAGGGCGGCTCGCT 657
 DB 265 ACCAGTAAACCTCAGACATCAGAGAACCTTATTCGGAGAGGTGAGGGCGGCTCGCT 324
 OY 658 GGGAGCTACTCAGAAATGAGAGATGACGGCGGCTTCACTCCCTGGTGGAAACAAATA 717
 DB 325 GGGAGCTACTCAGAAATGAGAGATGACGGCGGCTTCACTCCCTGGTGGAAACAAATA 384
 OY 718 GATCCTCAGTCAATGATATATACCAAGTCAATGGCTTTTGGTAAATCTCCATCT 777
 DB 385 GATCCTCAGTCAATGATATATACCAAGTCAATGGCTTTTGGTAAATCTCCATCT 444
 OY 778 CCAATTTTACATATATACCAAGTCAATGGCTTTTGGTAAATCTCCATCT 837
 DB 445 CCAATTTTACATATATATACCAAGTCAATGGCTTTTGGTAAATCTCCATCT 504
 OY 838 CTACTATACGAGTTTATATATATACCAATGCTACAGAAAGCAAGATGTTATGA 897
 DB 505 CTACTATACGAGTTTATATATATATACCAATGCTACAGAAAGCAAGATGTTATGA 564
 OY 898 GGGGCTCAGAGAGGGGTTGAATGCTTAACACCACTCAGTCTGTTAGT 957
 DB 565 GGGGCTCAGAGAGGGGTTGAATGCTTAACACCACTCAGTCTGTTAGT 624
 OY 958 GCTGAATATATATGCGCCATGTTAGACAGAAAGTCAAGAGTCAAGATGTTG 1017
 DB 625 GCTGAATATATATGCGCCATGTTAGACAGAAAGTCAAGAGTCAAGATGTTG 684
 OY 1018 GAAATTCACAGA 1029
 DB 685 GAAATTCACAGA 696
 RESULT 12
 AAD27814
 ID AAD27814 standard; DNA: 645 BP.
 AC AAD27814;
 XX 18-APR-2002 (first entry)
 DE Human cytokine receptor gene, sbg456548cytoRa #1.
 XX
 XX Human; therapy; wound healing disorder; vaccine; cancer; infection;
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarhythmic;
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
 KW ischemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
 KW depression; cardiovascular disease; myocardial infarction; renal failure;
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
 KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
 KW neotropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;


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FT      /product= "Human DNAX cytokine receptor subunit 4.1
FT      (DCRS4.1)"
FT      sig_peptide      1..63
FT      mat_peptide      64..747
FT      /tag= b
FT      /tag= c
FT      /product= "Human mature DNAX cytokine receptor
FT      subunit 4.1 (DCRS4.1)"
XX
XX      WO200136467-A2.
XX
XX      25-MAY-2001.
XX
XX      16-NOV-2000; 2000WO-US31363.
XX
XX      18-NOV-1999; 99US-0443060.
XX      13-DEC-1999; 99US-0170320.
XX
XX      (SCHE ) SCHERING CORP.
XX
XX      Gorman DM;
XX
XX      MPI: 2001-343800/36.
XX      P-PSDB: AAE02458.
XX
XX      New mammalian receptor proteins related to cytokine receptors, useful
XX      for regulating cell development and for diagnosis and treatment of
XX      immunological disorders
XX
XX      Claim 16; Page 21-22; 124pp; English.
XX
XX      The present sequence is human DNAX cytokine receptor subunit 4.1
XX      (DCRS4.1) cDNA. DCRS4 gene is located on chromosome 6q24.1-25.2.
XX      Cytokine receptors, fragments and antibodies are useful for treating
XX      immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
XX      useful in drug screening to identify compounds having binding affinity
XX      to the receptor subunit. Modulators of DCRs are useful for modulating
XX      the physiology or development of a cell or tissue culture cells. A
XX      purified DCRS is useful as a reagent to detect antibodies generated in
XX      response to the presence of elevated levels of expression, or
XX      immunological disorders which lead to production of antibody to the
XX      endogenous receptor. Cytokine receptor sequences are useful as probes
XX      for detecting levels of the cytokine receptor in patients suspected of
XX      having an immunological disorder. Antibodies have therapeutic value, are
XX      useful as potent antagonists, in detecting or quantifying ligands, for
XX      isolating DCRs proteins and peptides, to screen expression libraries for
XX      particular expression products, to raise anti-idiotypic antibodies and
XX      for detecting or diagnosing various immunological conditions related to
XX      expression of the protein or cells which express the protein.
XX
XX      Sequence 750 BP; 259 A; 147 C; 164 G; 180 T; 0 other:
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XX      Query Match      34.1%; Score 449.2; DB 22; Length 750;
XX      Best Local Similarity 76.6%; Pred. No. 1.4e-83;
XX      Matches 607; Conservative 0; Mismatches 143; Indels 42; Gaps 3;
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XX      1 ATGATGCTTAACATGTGTTCTAGGCTTCTCATCAGTCTTCTTCTACTGCTGAGCA 60
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XX      298 GGAAGCTCAGTACAGCAGTCTCTGAGGCTCAGAGGCTCAATTTTCAGTCCGGAAT 357
XX      61 GGAAGCTCAGTACAGCAGTCTCTGAGGCTCAGAGGCTCAATTTTCAGTCCGGAAT 120
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XX      358 TTTCACAACATTTTGCAATGGCAGGCTGGAGGCGACTTACTGGCAACAGCAGTGTAT 417
XX      121 TTTCACAACATTTTGCAATGGCAGGCTGGAGGCGACTTACTGGCAACAGCAGTGTAT 180
XX
XX      418 TTTCGAGCTCAAAATGATGTTCTCATGAGCAGTCAAGTAAGCTTCACAGCAAGCAAGT 477
XX      181 TTTCGAGCTCAAAATGATGTTCTCATGAGCAGTCAAGTAAGCTTCACAGCAAGCAAGT 239
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DB      240 TACTCAGAACTCTCTTGTGACCTTACCACTGAAACCTCAGCATACAGAACTTATTA 299
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XX      300 CGGGAGGAGGGGCAAAATTAATAAATAAG-----GGAATCCCTTGGGGCCAA 347
XX
XX      598 ACCAGTGAACCTCAGACATACAGGAACCTTATTTACGGGAGGGGTAGGGCGGCTCGCT 657
XX      348 ACAAGTAAGCAAGAAATCAAAAGGGAGACCAGA----- 379
XX
XX      658 GGGAGCTTACAGATGAGCATGACGCCGCTTACCTCCCTGGTGGGAAACAAAATA 717
XX      380 -AGACCAACACAGTACGTCCGCCAGCTGCCGCAAGGCAATTTGCGAGTGCAGAAAATA 438
XX
XX      718 GATCCTCAGTCATGATTAATTAACCAAGTCAATGCTCTTTGTTGTAATTCCTCATGCT 777
XX      439 GATCCTCAGTCATGATTAATTAACCAAGTCAATGCTCTTTGTTGTAATTCCTCATGCT 498
XX
XX      778 CCAATTTACCTATAGATTAACCAAGAAAGAAATGTAATCTATAGAAATTTACTATGAA 837
XX      499 CCAATTTACCTATAGATTAACCAAGAAAGAAATGTAATCTATAGAAATTTACTATGAA 558
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XX      838 CTACTATACCGAGTTTATTAATTAACCAATTCATAGAAAGAGGAGGTTATGAA 897
XX      559 CTACTATACCGAGTTTATTAATTAACCAATTCATAGAAAGAGGAGGTTATGAA 618
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XX      619 GGGGCTCAGAGCGGTTAAATTAAGCTCTTAACCAACACACTCCAGCTACCTGTAAGT 678
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XX      08-AUG-2002 (first entry)
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XX      ulcerative colitis; transplant rejection; abortion; antipsoriatic;
XX      immunosuppressive; antineumatic; antiarthritic; neuroprotective;
XX      antiinflammatory; antitumor; cytosolic; dermatological;
XX      chromosome 6q24.1-25.2; receptor; gene; ss.
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XX      EP1191035-A2.
XX
XX      24-AUG-2001; 2001EP-0250307.
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XX      25-SEP-2000; 2000DE-1048626.
XX      17-NOV-2000; 2000DE-1058907.
XX      19-DEC-2000; 2000DE-1064906.

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XX (SCHD) SCHERING AG.
 XX
 PI Weiss B, Sabat R, Assadullah K, Toshi L;
 XX WPI: 2002-333210/37.
 DR P-PSDB: AAO17380.
 XX
 PT New nucleic acid encoding soluble cytokine receptor, useful for
 PT diagnosis and treatment of e.g. immune disease, also related protein
 PS and antibodies
 XX
 PS
 CC Claim 1; Page 12; 21pp; German.
 CC
 CC The present invention provides the protein and coding sequences of 3
 CC variants of a human cytokine receptor. The sequences can be used in the
 CC diagnosis, prevention and treatment of immune diseases, including
 CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
 CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
 CC transplant rejection and in reproductive medicine, e.g. for diagnosing
 CC the coding sequence of variant 1 of the invention.
 XX
 SQ Sequence 750 BP; 259 A; 147 C; 164 G; 180 T; 0 other;
 Query Match 34.1%; Score 449.2; DB 24; Length 750;
 Best Local Similarity 76.6%; Pred. No. 1.4e-83;
 Matches 607; Conservative 0; Mismatches 143; Indels 42; Gaps 3;
 OY 238 ATGATGCTTAACCATTTGCTTCTAGAGCTTCCTCATGTTCTCTCTCTGTTAGCA 297
 DB 1 ATGATGCTTAACCATTTGCTTCTAGAGCTTCCTCATGTTCTCTCTCTGTTAGCA 60
 OY 298 GGAAGCTGCAACCATGAGTCTCTGAAGCCTCAGAGGGTACAAATTTGCTCCGAAAT 357
 DB 61 GGAAGCTGCAACCATGAGTCTCTGAAGCCTCAGAGGGTACAAATTTGCTCCGAAAT 120
 OY 358 TTTTCAACATTTTTCATGAGCAGCTGGAGGGGCACTTACGCAAGCAGCTGTCTAT 417
 DB 121 TTTTCAACATTTTTCATGAGCAGCTGGAGGGGCACTTACGCAAGCAGCTGTCTAT 180
 OY 418 TTTTGCAGTACAAATATGTTCTCATGAGCATGAAAGCTCTCACCAGAGCAAGT 477
 DB 181 TTTTGCAGTACAAAT-ATATGACAGACAAATGAAATATAAGAAAGCTGTGGGG 239
 OY 478 GGATGCTGGCAGCATTTCTTGAATTCCTCCAGGCTCAGAACTTGGCTTAATATGGA 537
 DB 240 TACTCAGAACTCTCTGTGTGACCTTACAGTGAACCTCAGACATACAGAACTTATTA 299
 OY 538 CAGAGACATGGAATAAATAAGAGACTGTGGGGTACTCAAGAACTCTGTGACCTT 597
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 DB 348 ACAAGATTAACGGAATCAAAAGGGGAACAGA-----379
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 OY 718 GATCTCCATGATGAATTAACCAAGTAATGCTCTTGTGGTGAATTTCTCATGCT 777
 DB 439 GATCTCCATGATGAATTAACCAAGTAATGCTCTTGTGGTGAATTTCTCATGCT 498
 OY 778 CCAATTTACCATATGATACCAAAAGAAAAAATGTATCTATAGAAAGTTACTATGAA 837
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OY 898 GGGGCTCAGAGCGGTTGAATGAGCTTAACACCACTCCAGCTACTGTAGTG 957
 DB 619 GGGGCTCAGAGCGGTTGAATGAGCTTAACACCACTCCAGCTACTGTAGTG 678
 OY 958 GCTGAATATATACGCCCATGTTAGACAGAAAGTCAAGAGTCAAGAGTGTG 1017
 DB 679 GCTGAATATATACGCCCATGTTAGACAGAAAGTCAAGAGTGTG 738
 OY 1018 GAAATTCATGA 1029
 DB 739 GAAATTCATGA 750
 RESULT 15
 AAD06415
 ID AAD06415 standard; DNA: 693 BP.
 XX
 AC AAD06415:
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Human DNA cytokine receptor subunit 4.2 reverse translational DNA.
 XX
 KW Human: immunomodulator; DNA cytokine receptor subunit 4.2; DCRS4.2;
 KW therapy; immunological disorder; drug screening; cell development;
 KW chromosome 6q24.1-25.2; ds.
 OS Homo sapiens.
 OS
 PN WO200136467-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000: 2000WO-US31363.
 XX
 PR 18-NOV-1999: 99US-0443060.
 PR 13-DEC-1999: 99US-0170320.
 XX
 PA (SCHE) SCHERING CORP.
 PI Gorman DM:
 XX
 DR WPI: 2001-343800/36.
 XX
 PT New mammalian receptor proteins related to cytokine receptors, useful
 PT for regulating cell development and for diagnosis and treatment of
 PT immunological disorders
 PS
 PS Disclosure: Page 25; 124pp; English.
 XX
 CC The present sequence is human DNA cytokine receptor subunit 4.2
 CC (DCRS4.2) reverse translational DNA. DCRS4 gene is located on
 CC chromosome 6q24.1-25.2. Cytokine receptors, fragments and antibodies are
 CC useful for treating immunological disorders. DCRS3 (50R), DCRS4 (cytor)
 CC or fragments are useful in drug screening to identify compounds having
 CC binding affinity to the receptor subunit. Modulators of DCRS are useful
 CC for modulating the physiology or development of a cell or tissue culture
 CC cells. A purified DCRS is useful as a reagent to detect antibodies
 CC generated in response to the presence of elevated levels of expression,
 CC or immunological disorders which lead to production of antibody to the
 CC endogenous receptor. Cytokine receptor sequences are useful as probes
 CC for detecting levels of the cytokine receptor in patients suspected of
 CC having an immunological disorder. Antibodies have therapeutic value, are
 CC isolating DCRS proteins and peptides, to screen expression libraries for
 CC particular expression products, to raise anti-idiotypic antibodies and
 CC for detecting or diagnosing various immunological conditions related to
 CC expression of the protein or cells which express the protein.
 XX
 SQ Sequence 693 BP; 131 A; 70 C; 108 G; 93 T; 291 other;
 Query Match 30.2%; Score 398.2; DB 22; Length 693;
 Best Local Similarity 51.0%; Pred. No. 4.9e-73;

Matches 402; Conservative 179; Mismatches 111; Indels 96; Gaps 1;

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Db 1 ATGATGCCCAARCAATGCTTCTTAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 60
OY 298 GGAACCTCAGTCAACGATGATGCTCTGGAAGGCTGAGGCTGACATTTCAATCCCAAT 357
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Db 61 GGNACNCARMSNACAYGARMSNYTNAARCCARMSNGTNCARITTYCARMSMGNAY 120
OY 358 TTTGACACATTTTGCATGAGCCTGAGGAGGCTTACTGCAACAGCATGTCTAT 417
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Db 121 TTYCATAAATHTHTNCARITGCAACGNGMNGCNYTNACNGMAAYMSMNGTNTAY 180
OY 418 TTTGTCAGTCAAAATCATGTTCTCATGCACTGAAAGCTCTCACCAAGCCAGT 477
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OY 478 GGATGCTGGAGCAGCATTTCTTGAATCTCCAGGCTGAGAACATTTGCTAAATATGCA 537
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Db 198 -----HTAYGNN 204
OY 538 CAGAGACATGAAAAATAAAGAACTGTTGGGTACTCAAGAACTCTTGTGACCT 597
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Db 325 GGNMSNTAYMSNGARTGASNTAGCNCNMNTTAYACNCCNTGTTGGGAGACNAARATH 384
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OY 778 CCAATTTACATATAGATACCAAGGAAAAAATGATCTATAGAGATTTACTATGAA 837
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Job time : 265 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
10840.859 Million cell updates/sec

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Sequence: 1 cagttcttcacatcgttaca.....aaaaaaaaaaaaaaaaaaaaa 1318

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Searched: 16154066 seqs, 8097743376 residues
1 number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: em_estcpl:*
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9: gb_est1:*
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13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	284.4	21.6	632	10	BB636466
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4	160	12.1	572	10	BB637530
5	124.2	9.4	494	12	BE809214
6	106.2	8.1	548	17	BH117626

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c	11	76.2	5.8	454	9	AL513951	AL513951
c	12	75.8	5.8	304	9	AL514919	AL514919
c	13	75.4	5.7	319	9	AL513977	AL513977
c	14	75.2	5.7	365	9	AL515373	AL515373
c	15	74.4	5.6	503	9	AL513809	AL513809
c	16	74.2	5.6	366	9	AL514543	AL514543
c	17	74.2	5.6	794	17	A2530415	A2530415
c	18	74	5.6	240	9	AU074171	AU074171
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c	24	73	5.5	401	9	AL515191	AL515191
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c	26	73	5.5	638	9	AL513901	AL513901
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c	28	72.4	5.5	449	9	AL513998	AL513998
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c	31	71.8	5.4	601	9	AL513631	AL513631
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c	37	71.2	5.4	425	9	AL514791	AL514791
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c	41	71	5.4	313	14	BQ391420	BQ391420
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ALIGNMENTS

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DEFINITION AV714177 DCB Homo sapiens cDNA clone DCBAMP09 5', mRNA sequence.
ACCESSION AV714177
VERSION AV714177.1 GI:10795694
KEYWORDS
SOURCE
ORGANISM

Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 698)
XU,X., GU,J., LIU,F., OU,J., ZHAO,M., LI,Y., HUANG,Q., ZHOU,J.,
SONG,H., GU,Y., YANG,Y., GAO,G., XIAO,H., LI,N., QIAN,B., GAO,X.,
CHENG,Z., XU,S., GU,W., TU,Y., JIA,O., FU,G., REN,S., ZHONG,M., LU
G., CHENG,Z., and Han,Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
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/organism="Homo sapiens"

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DEFINITION	214608 MRC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION	BEB09214
VERSION	BEB09214.1 GI:10240317
KEYWORDS	EST,
SOURCE	COW,
ORGANISM	Bos taurus

REFERENCE
AUTHORS
1 (bases 1 to 494)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertege,G., Holt,I.I., Karamycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.
TITLE
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL
Genome Res. 11 (4), 626-630 (2001)
EDLINE
21180013
CONTACT
Contact: Smith TPL

PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.960904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACGATGTACCAT
BACKWARD: GTTTTCCGAGTCACGACG
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Location/Qualifiers
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source

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Library made from pooled tissue from testis, thymus,
semiteadonous muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

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Best Local Similarity		79.5%,	Pred. No. 1.8e-09;	
Matches 147; Conservative		0;	Mismatches 38;	Indels 0; Gaps 0;
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QY	587	CTGTGTGACCTTAACCAAGTGAACCTCAGACATCAGAGAACTTATTACGGAGAGGTGAGGG	646	
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QY	647	CGGCTTCGGCTGTGGAGCTACTCAGATGAGCATGACGCGCGGTTTCACTCCCTGGTGG	706	
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BH117626/c	
LOCUS	BH117626
DEFINITION	BH117626 548 bp DNA linear GSS 19-JUL-2001 RPCT-24-253122.TV RPCT-24 Mus musculus genomic clone RPCT-24-253122 , DNA sequence.
ACCESSION	BH117626
VERSION	BH117626
KEYWORDS	GSS. GI:14959077
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Zhao, S., Niemman, W., Malek, J., Shatsman, S., Aktinur, B., Levins, M., Tsagaris, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.	Mouse BAC End Sequences from Library RPc1-24	Unpublished (1999)	Other-GSSS: RPc1-24-253122.TJ

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (dejong@gmail.com). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 253 row: I column: 22
Seq primer: T7
Class: BAC ends.

```

FEATURES:
Source
Location/Qualifiers
1. .548
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-253122"
/clone_1lb="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pPRABAC1; Site_1: BamHI; Site_2: BamHI; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pPRABAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."
BASE COUNT
182 a 85 c 100 g 181 t

```

ORIGIN		Query Match	8.1%;	Score 106.2;	DB: 17;	Length 548;
		Best Local Similarity	75.4%;	Pred. No. 8.1e-07;		
Matches	132;	Conservative	0;	Mismatches 43;	Indels	0;
					Gaps	0;
QY	708	ACACAAATATACATCTCCAGTCATGAAATTAACCCAGTCATGGCTCTTTGGTAAAT				
Db	229	AGCAAACTATACTCTCTCCGTCGTGACATATACCCGAAATTAACGATCTTTGGCGGTCT				
QY	768	TCTCCATGCTCCAATTATACCATATAGATTACCAAAAGAAAAAATGTATCTATAGAGA				
Db	169	TAAACGTCTCTCAGAGTTGCCAAATAGAAACCAAGTGGAAAAATTTGATCATCGAAGAC				
QY	828	TTATCATATACATACATACCGAGTTTATATATTAACATTCACATAGAGAAAGAG				
Db	109	TTACTAGCGCTTAGATATACAGAGTTTTCACAAATCAACATTCACATAGAGAAAGTG				

COLT 7	22045/c	645 bp	DNA	linear	GSS 24-JAN-2001
DEFINITION	Mus musculus genomic clone RPCI-24-140H15				
ACCESSION	AF722045				
VERSION	AF722045				
KEYWORDS	RPCI-24-140H15.TV RPCI-24 Mus musculus				
SOURCE	GSS.				
ORGANISM	house mouse.				
	Mus musculus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 645)				
AUTHORS	Zhao, S., Nleman, W., Malek, J., Shatsman, S., Akintet, B., Levins, M.,				

REFERENCE
AUTHORS
1 (bases 1 to 645)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akiror, B., Levins, M.,
Tesdare, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregiorgis, E.,
Russell, D., de Jong, P. and Fraser, C. M.,
Mouse BAC End Sequences from Library RPCT-24
Unpublished (1999)
- JOURNAL
- COMMENT
Contact: Shaying Zhao

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhac@tigr.org
Clones are derived from the mouse BAC library RPECI-24. For BAC library availability, please contact Pieter de Jong (pdejong@small.chu.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderingframe.htm>). BAC end sequence: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 140 row: H column: 15
Seq primer: T7
Class: BAC ends.

FEATURES	SOURCE	Location/Qualifiers
		1. 645
		/organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="taxon:10090"
		/clone="RPCT-24-140H15"
		/clone_lib="RPCT-24"
		/sex="Male"
		/cell_type="Spleen/Brain"
		/note="Vector: pTARBAC1; Site_1: BamHI; Site_2: BamHI; RPCT-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."
BASE COUNT	191 a	156 c 121 g 177 t
ORIGIN		

Query Match	6.48;	Score 84.6;	DB 17;	Length 645;
Best Local Similarity	73.5%;	Pred. No. 0.0012;		
Matches 108; Conservative	0;	Mismatches 39;	Indels 0;	Gaps 0

QY	288	TGGTGTGACAGAACTCAGTCAACAGCATGAGTCTCTAAGGCTCAGAGGGGTACAAATTTC	347
	111		111
Db	642	TGCTGCTTAAAAATTAACACAGCTCGTATCTCTACGCGCCACGAAGGTCACATTTC	583
QY	348	GTCGCCAAATTTTACACAATTTTTGCATAGGACACCTGGGAGGCACTTTACTGGCAGCAG	407
	111		111
Db	582	GTCGCAAAATTTCCACAATTTTTGCACCTGGCAGCAGGAGCGTCTCTCCGACGACAA	523
QY	408	CAGTGTCTATTTTGTGCAGTCAAAAT	434
	111		111
Db	522	CAGCATCTACTTTGTGCAGTCAAGAA	496

RESULT	8
AM833620/c	
LOCUS	AM833620 583 bp mRNA linear EST_18-MAY-2000
DEFINITION	OYA-TT00008-161199-033-e05 TT0008 Homo sapiens cDNA, mRNA sequence.
ACCESSION	AM833620
VERSION	AM833620.1 GI:7927594
KEYWORDS	EST.
SOURCE	human.

ORGANISM	REFERENCE
Homo sapiens	
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.	
1 (bases 1 to 583)	
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.L.	
AUTHORS	

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G.

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAFESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/getthml2.pl?tl1=8t2-QV4-TT0008-161>)
199-033-e058t3-1999-11-16&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 578.

FEATURES	source	Location/Qualifiers
		1..583
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone_lib="TT0008"
		/dev_stage="Adult"
		/note="Organ: testis; Vector: puc18; Site_1: Sma1; Site_2: Sma1. A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 1966,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT		173 a 129 c 123 g 158 t
ORIGIN		

Query Match Similarity 6.1%; Score 81; DB 10; Length 583;
 Best Local Similarity 89.7%; Pred. No. 0.0045;
 Matches 87; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 288 TGCCTACGAGAACTCATACGCATGACGCTCTGMAAGCCTCAGAGCTCAATTCA 347
 DB 100 TTTTATCTTAGAATCTCATACGCATGAGTCTCTGAGAGCCTCAGAGGTCATATTCA 41

[illegible]

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES	Location/Qualifiers
Source	1. 311 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="Cl0BA006ZC11" /clone_lib="LTI_NF1006_PL2" /tissue_type="placenta" /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-Oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT	121 a 5 c 4 g 162 t 19 others
ORIGIN	
Query Match	5.8%; Score 77; DB 9; Length 311;
Best Local Similarity	55.3%; Pred. No. 0.026;
Matches 119; Conservative. 13; Mismatches 83; Indels 0; Gaps 0;	
Oy 1104	TCTATTTAAATGTTTGTATTTCTTAAGAATATTCATGTTACACCTTGGGA 1163
Db 67	TTT 126
Oy 1164	CTCTCTTTTATTCATCTTTTATTCCTTTATTTTCATTTGTAACATATTTGAACA 1223
Db 127	TTT 186
Oy 1224	CATTCGCCCGCAAAATGAAATGAAGATGAGGACAGAAATTAAGTGTCTATGAAA 1283
Db 187	AAAWAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAARRRRRAGRRGARRA 246
Oy 1284	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
Db 247	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 281
RESULT 11	
AL513951/c	454 bp mRNA linear EST 13-FEB-2001
LOCUS	AL513951 LTI_NF1006_PL2 Homo sapiens cDNA clone Cl0BA0102D12 3
DEFINITION	prime, mRNA sequence.
ACCESSION	AL513951
VERSION	AL513951.1 GI:12777445
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France

FEATURES Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers

1. 454

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CLOB0102D12"

/clone_1lb="LTI_NFL006_PL2"

/tissue="placenta"

/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 226 a 33 c 26 g 127 t 42 others

Query Match 5.8%; Score 76.2; DB 9; Length 454;

Best Local Similarity 53.1%; Pred. No. 0.027; Indels 0; Gaps 0;

Matches 120; Conservative 15; Mismatches 91; Indels 0; Gaps 0;

Db 1093 TGTGGAAGACATCTTATTAATGTTTCTTAAAGCAATATTCACGTGA 1152

277 TTTTGGGGGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCC 218

Qy 1153 CACCTGGGGAAGCTCTTGTGTTATCCATTCTTATATTTCAATTTGTAACGA 1212

217 CCYTTT 158

Db 1213 TATTTGACGACATCCCGGCAAAATGAATGAATGAGCAGACAGATAAGG 1272

157 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 98

Qy 1273 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1318

97 AA 52

RESULT 12

AL514919/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 304

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CLOB0122F06"

/clone_1lb="LTI_NFL006_PL2"

/tissue="placenta"

/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 134 a 5 c 8 g 151 t 6 others

Query Match 5.8%; Score 75.8; DB 9; Length 304;

Best Local Similarity 58.1%; Pred. No. 0.04; Indels 0; Gaps 0;

Matches 125; Conservative 4; Mismatches 86; Indels 0; Gaps 0;

Db 1104 TCTTATTAATTAATGTTTGTATTTCTTAAGCAATATTCACGTGACCTGGGA 1163

276 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 217

Qy 1164 CTCTTGTGTTTATTCATCTTTTATCCATTCTTATATTTCAATTTGTAACGA 1223

216 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 157

Db 1224 CATTCCCGGCAAAATGAATGAATGAGCAGACAGATAAGTGTCTATGAAA 1283

156 AAAAAAACAACAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 97

Qy 1284 AA 1318

96 AA 62

RESULT 13

AL513977/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 319

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CLOB0112F09"

/clone_1lb="LTI_NFL006_PL2"

/tissue="placenta"

/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 150 a 12 c 7 g 148 t 2 others

Query Match 5.7%; Score 75.4; DB 9; Length 319;

Best Local Similarity 59.1%; Pred. No. 0.044; Indels 0; Gaps 0;

Matches 127; Conservative 1; Mismatches 87; Indels 0; Gaps 0;

QY 1104 TCTTATTAATGTTTGTATTTTCTTAAGCAATATTCAGTACCTGGGA 1163
 Db 263 TTTTATTTTATTTTATTTTATTTTATTAACCTTTTATTTTATTTTATTTT 204
 QY 1164 CTCTGTTTATTCATCTTTATTCCTTTATTTATTTGATTTGAACGA 1223
 Db 203 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 144
 QY 1224 CATTCCTCCGCAAAATGAATGAAGATGAGCAGAGATTAAGTCTTATGAAA 1283
 Db 143 TTTTATTAATAAATAATTAATAAATAAATAAATAAATAAATAAATAAATAA 84
 QY 1284 AA 1318
 Db 83 AA 49

RESULT 14
 AL515373/c 365 bp mRNA linear EST 13-FEB-2001
 DEFINITION AL515373 LTI_NFL006_P12 Homo sapiens cDNA clone Cl08B017ZD11.3
 prime, mRNA sequence.
 ACCESSION AL515373
 VERSION AL515373.1 GI:12778866
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 365)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 SOURCE Location/Qualifiers
 1..365

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Cl08B017ZD11"
 /clone_lib="LTI_NFL006_P12"
 /tissue_type="Placenta"
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email: filang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 100 a 5 c 6 g 230 t 24 others

Query Match 5.7%; Score 75.2; DB 9; Length 365;
 Best Local Similarity 53.8%; Pred. No. 0.044; Mismatches 113; Conservative 17; Indels 0; Gaps 0;

QY 1109 TTTAAATGTTTGTATTTCTTAAGCAATATTCAGTACCTGGGACTTCT 1168
 Db 297 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 238
 QY 1169 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1228
 Db 237 ATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 178
 QY 1229 CCCCCGAAATGAATGAAGATGAGCAGAGATTAAGTCTTATGAAAAA 1288
 Db 177 AAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 118

QY 1289 AA 1318
 Db 117 AAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 88

RESULT 15
 AL513809/c 503 bp mRNA linear EST 13-FEB-2001
 LOCUS AL513809 LTI_NFL006_P12 Homo sapiens cDNA clone Cl08A009ZF09.3
 DEFINITION prime, mRNA sequence.
 ACCESSION AL513809
 VERSION AL513809.1 GI:12777303
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 503)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 SOURCE Location/Qualifiers
 1..503

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Cl08A009ZF09"
 /clone_lib="LTI_NFL006_P12"
 /tissue_type="Placenta"
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email: filang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 138 a 144 c 4 g 133 t 84 others

Query Match 5.6%; Score 74.4; DB 9; Length 503;
 Best Local Similarity 43.4%; Pred. No. 0.048; Mismatches 98; Conservative 45; Indels 83; Gaps 0;

QY 1093 TGTGAAGATCTTATTAATGTTTGTATTTCTTAAGCAATATTCAGTGA 1152
 Db 267 TTKTKKKKGGGGGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 208
 QY 1153 CACCTGGGACTCTTGTATTCATTTTATTCCTTATTTATTTGTAACGA 1212
 Db 207 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 148
 QY 1213 TATTTGAAGCATCTCCCGGCAAAATGAAGTGAAGTGAAGCAGAGATTAAGTG 1272
 Db 147 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 88
 QY 1273 TTTGATGAAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1318
 Db 87 AA 42

Search completed: December 22, 2002, 09:11:13
 Job time : 1977 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 22, 2002, 07:44:21 ; Search time 55 Seconds
(Without alignments)
7349.090 Million cell updates/sec

Title: US-09-964-994-1

Perfect score: 1318
Sequence: 1 cagttcttcacgtcgaac.....aaaaaaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY_NMC
Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 15338381 residues

1 number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/prodata/1/ina/5a_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5b_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6a_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6b_COMB.seq:*
5: /cgn2_6/prodata/1/ina/pctus_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69.2	5.3	1659	2	US-08-943-087-45
2	68.6	5.2	1659	2	US-08-943-087-13
3	68.6	5.2	1659	2	US-08-943-087-31
4	68	5.2	1659	2	US-08-943-087-19
5	67.8	5.1	663	2	US-08-943-087-53
6	67	5.1	663	2	US-08-943-087-49
7	67	5.1	663	2	US-08-943-087-51
8	67	5.1	1659	2	US-08-943-087-15
9	67	5.1	1659	2	US-08-943-087-17
10	67	5.1	1659	2	US-08-943-087-23
11	67	5.1	3516	2	US-08-943-087-1
12	66.8	5.1	1659	2	US-08-943-087-25
13	66.4	5.0	1659	2	US-08-943-087-21
14	65.4	5.0	663	2	US-08-943-087-57
15	65.4	5.0	1659	2	US-08-943-087-29
16	65.4	5.0	1659	2	US-08-943-087-29
17	64.2	4.9	663	2	US-08-943-087-39
18	64.2	4.9	1659	2	US-08-943-087-59
19	63.8	4.8	663	2	US-08-943-087-37
20	63.8	4.8	1659	2	US-08-943-087-55
21	63.8	4.8	1659	2	US-08-943-087-41
22	63.6	4.8	1659	2	US-08-943-087-43
23	63.2	4.7	1659	2	US-08-943-087-27
24	61.4	4.7	6671	1	US-08-943-087-33
25	61.4	4.7	6671	1	US-08-280-443-1
26	61.4	4.7	6671	1	US-08-457-459-1
27	61.4	4.7	6671	5	US-08-555-678-1
					Pct-US95-02275-1

28	61	4.6	1659	2	US-08-943-087-35	Sequence 35, Appl
29	60.8	4.6	3602	4	US-09-402-929-1	Sequence 1, Appl
30	58.6	4.4	5852	1	US-07-867-106-2	Sequence 2, Appl
31	56.4	4.3	1129	4	US-09-227-357-40	Sequence 40, Appl
32	55.8	4.2	1659	2	US-08-943-087-47	Sequence 47, Appl
33	55	4.2	578	4	US-09-602-877A-95	Sequence 95, Appl
34	54.8	4.2	1411	4	US-08-964-127-5	Sequence 5, Appl
35	54.8	4.2	1411	4	US-09-496-692-5	Sequence 5, Appl
36	54.6	4.1	882	2	US-08-909-965C-9	Sequence 9, Appl
37	54.6	4.1	6476	4	US-09-127-670-5	Sequence 5, Appl
38	54.4	4.1	1474	4	US-08-821-994-64	Sequence 64, Appl
39	54.2	4.1	1582	3	US-08-545-196B-10	Sequence 10, Appl
40	54.2	4.1	1382	3	US-08-545-196B-12	Sequence 12, Appl
41	54.2	4.1	2246	4	US-09-363-708-3	Sequence 3, Appl
42	54.2	4.1	2447	2	US-09-014-969-14	Sequence 14, Appl
43	54	4.1	1507	4	US-09-453-323-1	Sequence 1, Appl
44	53.6	4.1	2852	3	US-09-027-137-2	Sequence 2, Appl
45	53.6	4.1	2852	4	US-09-344-441-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-943-087-45
; Sequence 45, Application US/08943087
; Patent No. 5945311
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Fairah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1659 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1659

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1659
OTHER INFORMATION:
US-08-943-087-31

Query Match 5.2%; Score 68.6; DB 2; Length 1659;
Best Local Similarity 51.8%; Pred. No. 4.4e-07;
Matches 155; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

529 AATATGACAGACATGGAATAAAGACGCTGGGGTACTCAGAACTCTCT 588
|||||
223 ATATATGGGCAAGAAATGGCTGAATTAATCAGAAATATCATAGAACCTAC 282
|||||
589 TGTGACCTTACCACTGAACCTCAGACATACAGGAACCTTATACGGGAGGCG 648
|||||
283 TGTGACCTTCTCTGTAACCTTCTGACAGACACAGATTTATGCCAAGTTTAGGCC 342
|||||
649 GCTCGGCTGGAGCTACATGAGATGAGCATGACGCCGGCTTACTCCTGTGGGAA 708
|||||
343 ATTGGGGAACAAAGTCTTCAATGGCTGAAAGTGAGAGTCTCTCTTTTGGAA 402
|||||
709 ACAAAATAGATCCTCCAGTCAATATATACCAAGTCAATGCTCTTTTGTATAT 768
|||||
403 ACACAATATGGCCACACAGAGTGCGCCTGACTACATGAGAGTCCATTTCTGTGTC 462
|||||
769 CTCACATGCTCCAAATTTACATATAGATACCAAAAGAAAAATGTATCTATAGAGA 827
|||||
463 CTGACAGCTCCAGAGAGTGAAGAGAAATCCAGAAAGACCTTCTGTTCCATGCACAA 521
|||||

RESULT 4

US-08-943-087-19
Sequence 19, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Whitmore, Robyn L.
APPLICANT: Fairah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1659
OTHER INFORMATION:
US-08-943-087-19

Query Match 5.2%; Score 68; DB 2; Length 1659;
Best Local Similarity 51.7%; Pred. No. 6.1e-07;
Matches 155; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

528 TAATATGACAGACATGGAATAAAGACGCTGGGGTACTCAGAACTCTC 587
|||||
222 TATATGAGCAAAAGAAATGGCTGAATTAATCAGAGTGCAGAAATCATAGAACCTA 281
|||||
588 TGTGACCTTACCACTGAACCTCAGACATACAGGAACCTTATACGGGAGGCTGAGGC 647
|||||
282 CTGTGATCTTCTGCTGAACCTTCTGATGACGACACACATATATGCCAAGTTAGGC 341
|||||
648 GGCCTCGGCTGGAGCTACTCAGATGAGCATGACGCCGGTTCACCTCCGCTGGTGA 707
|||||
342 CATTTGGGGAACAAGTGTCCAAATGGCTGAGAGTGGACGGTTTATCTTTTGA 401
|||||
708 AACAAATAGATCTCCAGTCAATATTAACCAAGTCAATGCTCTTTGTGTAAT 767
|||||
402 GACACAAATTTGGCCACACAGAGTGGCAGCTGACTACAGATGAGAGTCCATTTCTGTGT 461
|||||
768 TCTCCATGCTCCAAATTTCCATATATATACCAAAAGAAAAATGTATCTATAGAGA 827
|||||
462 CCGACAGCTCCAGAGAGTGAAGAGAAATCCAGAGACCTTCTGTTCCATGCACAA 521
|||||

RESULT 5

US-08-943-087-53
Sequence 53, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Whitmore, Robyn L.
APPLICANT: Fairah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...663
OTHER INFORMATION:
US-08-943-087-53

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```

Query Match 5.1%; Score 67.8; DB 2; Length 663;
Best Local Similarity 51.5%; Pred. No. 5.1e-07;
Matches 156; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

```

```

531 ATATGACGAGACATGGAATAAAGAGACTGTGGGCTACGACACTCTTG 590
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
138 ATATGGGCAAGAAAGTGTGTAATATGAAATGCAAAATATCATAGAACCTTG 197
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
591 TGACCTTACAGTACGACATACAGAACCTTATTACGGAGGGTGAAGGGCG 650
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
198 TGTATCTTTCCTGGAACCTTCTAGTACGAAACACAGTATATCCAAAGTTAAGCCAT 257
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
651 CTGGCTGGAGCTACTCAGATGAGCATGACGCGCGGCTTCACTCCCTGGTGGGAAC 710
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
258 TTGGGGAACAAGTGTCCCAATGAGGCTGAAAGTGAAGGTTCTATCTTTTGAAGAC 317
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
711 AAAAATGATCTCCAGTATGATATATACCAAGTCAATGGCTTGTGTAATCT 770
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
318 ACAATTTGGCCACGAGGTGGCAGTACGATGAGAGTCCATTTCTGTGTCT 377
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
771 CCATGCTCCAAATTTACATATAGATACCAAAAGAAAAATGATCTATAGAGATTA 830
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
378 GACAGCTCCAGAGAGTGAAGAAATCCAGAAAGCTTCTCTTCATGCAACAATTT 437
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
831 CTA 833
||
438 ATA 440

```

```

RESULT 6
US-08-943-087-49
; Sequence 49, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Rodyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrish, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle

```

```

STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...663
OTHER INFORMATION:
US-08-943-087-49

```

```

Query Match 5.1%; Score 67; DB 2; Length 663;
Best Local Similarity 51.5%; Pred. No. 7.9e-07;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

```

```

529 AATATGACGAGACATGGAATAAAGAGACTGTGGGCTACTGACGACTCTCT 588
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
136 ATATATGGGCAAGAAAGTGTGTAATATGAAATGCAAAATATCATAGAACCTTG 195
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
589 TGTGACCTTACAGTACGACATACAGAACCTTATTACGGAGGGTGAAGGGCG 648
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
196 TGTGATCTTTCCTGGAACCTTCTAGTACGAAACACAGTATATCCAAAGTTAAGCC 255
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
649 GCCTGGCTGGAGCTACTCAGATGAGCATGACGCGCGGCTTCACTCCCTGGTGGGA 708
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
256 ATTTGGGGAACAAGTGTCCCAATGAGGCTGAAAGTGAAGGTTCTATCTTTTGAAGAA 315
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
709 ACAAAATGATCTCCAGTATGATATATACCAAGTCAATGGCTTGTGTAATTT 768
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
316 ACACAATTTGGCCACGAGGTGGCAGTACGATGAGAGTCCATTTCTGTGTCT 375
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
769 CTGATGCTCCAAATTTACATATAGATACCAAAAGAAAAATGATCTATAGAGAA 827
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
376 CTGACAGCTCCAGAGAGTGAAGAAATCCAGAAAGCTTCTCTTCATGCAACA 434
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 7
US-08-943-087-51
; Sequence 51, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Rodyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrish, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR

```



```

? NUMBER OF SEQUENCES: 60
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Zymogenetics, Inc.
? STREET: 1201 Eastlake Avenue East
? CITY: Seattle
? STATE: WA
? COUNTRY: USA
? ZIP: 98102
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/943,087
? FILING DATE:
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/803,305
? FILING DATE: 20-FEB-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Lunn, Paul G
? REGISTRATION NUMBER: 32,743
? REFERENCE/DOCKET NUMBER: 96-24C1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 206-442-6627
? TELEFAX: 206-442-6678
? TELEX:
? INFORMATION FOR SEQ ID NO: 51:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 663 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: Coding Sequence
? LOCATION: 1..663
? OTHER INFORMATION:
?
US-08-943-087-51

Query Match
Best Local Similarity 5.1%; Score 67; DB 2; Length 663;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 529 AATATGACAGACAGACATGAAAAATTAAGAGACTGTGGGTACTCAAGACTCTCT 588
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 136 ATATATGGGCAAAAGAAATGCTGAATTAATCAGAAATATCAATAGAACCTAC 195
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 589 TGTGACCTTACCGAGTGAACCTCAGACATACAGGAACCTTATTAGGAGGCG 648
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 196 TGTGATCTTTCTGCTGAACCTTCTGACTGAAACACGAGTATTATGCCAAAGTTAAGCC 255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 649 GCCTGGCTGGAGCTACTCAGATGAGCATGACGCCGGGCTTCACTCCCTGGTGAA 708
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 256 ATTTGGGGAACAAAGTGTCCAAATGAGCGTGAAGTGACGGTCTTCTTTTGA 315
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 709 AAAAAATATGATCTTCACTGATGAATATTAACCAAGTCAATGGCTTTGTTGTAATT 768
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 316 ACACAATTTGGCCACACAGAGGTGGAGCTGACTACATGAGATGAGAAATTCATTTCTGTTGTC 375
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 769 CTCATGCTCCAAATTTTACATATATGATGACCAAGAAAGAAATATGATATATGAAGA 827
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 376 CTGACAGCTCCAGAGAGAGTGAAGAGAAATCCAGAAAGCTTCTGTTTCATGACACA 434
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 8
US-08-943-087-15

; Sequence 15, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.

```

? APPLICANT: Jelneberg, Anna C.
? APPLICANT: Adams, Robyn L.
? APPLICANT: Whitmore, Theodore E.
? APPLICANT: Farrah, Theresa M.
? TITLE OF INVENTION: CYTOKINE RECEPTOR
? NUMBER OF SEQUENCES: 60
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Zymogenetics, Inc.
? STREET: 1201 Eastlake Avenue East
? CITY: Seattle
? STATE: WA
? COUNTRY: USA
? ZIP: 98102
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/943,087
? FILING DATE:
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/803,305
? FILING DATE: 20-FEB-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Lunn, Paul G
? REGISTRATION NUMBER: 32,743
? REFERENCE/DOCKET NUMBER: 96-24C1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 206-442-6627
? TELEFAX: 206-442-6678
? TELEX:
? INFORMATION FOR SEQ ID NO: 15:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1659 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: Coding Sequence
? LOCATION: 1..1659
? OTHER INFORMATION:
?
US-08-943-087-15

Query Match
Best Local Similarity 5.1%; Score 67; DB 2; Length 1659;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 529 AATATGACAGACAGACATGAAAAATTAAGAGACTGTGGGTACTCAAGACTCTCT 588
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 223 ATATATGGGCAAAAGAAATGCTGAATTAATCAGAAATATCAATAGAACCTAC 282
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 589 TGTGACCTTACCGAGTGAACCTCAGACATACAGGAACCTTATTAGGAGGCG 648
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 283 TGTGATCTTTCTGCTGAACCTTCTGACTGAAACACGAGTATTATGCCAAAGTTAAGCC 342
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 649 GCCTGGCTGGAGCTACTCAGATGAGCATGACGCCGGGCTTCACTCCCTGGTGAA 708
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 343 ATTTGGGGAACAAAGTGTCCAAATGAGCGTGAAGTGACGGTCTTCTTTTGA 402
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 709 AAAAAATATGATCTTCACTGATGAATATTAACCAAGTCAATGGCTTTGTTGTAATT 768
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 403 ACACAATTTGGCCACACAGAGGTGGAGCTGACTACATGAGATGAGAAATTCATTTCTGTTGTC 462
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 769 CTCATGCTCCAAATTTTACATATATGATGACCAAGAAAGAAATATGATATATGAAGA 827
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 463 CTGACAGCTCCAGAGAGAGTGAAGAGAAATCCAGAAAGCTTCTGTTTCATGACACA 521
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 9

US-08-943-087-17

Db 403 ACACAAATGGCCACAGAGCTGACACTGACAGATGAGAGATCCATTGTGTGTC 462
QY 769 CTCGATGCTCAAAATTTACATATAGATACCAAGAAAATGATCTATAGAGA 827
Db 463 CTGACAGCTCCAGAGAGTGAAGAAATCCAGAAAGCTTCTGTTCCATGCAACA 521

RESULT 11

US-08-943-087-1
; Sequence 1, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:

APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087

FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3516 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 237...1895
OTHER INFORMATION:
US-08-943-087-1

Query Match 5.1%; Score 67; DB 2; Length 3516;
Best Local Similarity 51.5%; Pred. No. 1.3e-06;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 529 AATATGACAGACAGCAATGAATAAAGAGACTGTTGGGCTACTCAAGACTCTCT 588
Db 459 ATATATGGCCAAAGAAATGGCTGAATATCAATGCAAGAAATATCAATAGAACCTAC 518
QY 589 TGTGACCTTACCAAGTAACTCAGACATACAGAGACTTATTACGGGAGGTGAGGGCG 648
Db 519 TGTGATCTTTTGTGCGAAGCTTCTGACTACGAAACACAGATATATGCAAGTTAAGGCC 578

QY 649 GCTTCGGCTGGGAGCTACTCAGATGAGACGCGGCTTCCCTGCTGGGAA 708
Db 579 ATTTGGGGAACAAAGTGTTCAAATGGGCTGAAGTGGACGGTTCTATCCTTTTAGAA 638
QY 709 ACAAAATAGATCTCTCCAGTATGATATTAACCAAGTCAATGCTCTTTGTTGTAAT 768
Db 639 ACACAAATGGCCACAGAGTGGACACTGACATGAGATGAGAAAGTCATTCTGTTGC 698
QY 769 CTCGATGCTCCAAATTTACATATAGATACCAAGAAAATGATCTATAGAGA 827
Db 699 CTGACAGCTCCAGAGAGTGAAGAAATCCAGAAAGCTTCTGTTCCATGCAACA 757

RESULT 12

US-08-943-087-25
; Sequence 25, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:

APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087

FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1659
OTHER INFORMATION:
US-08-943-087-25

Query Match 5.1%; Score 66.8; DB 2; Length 1659;
Best Local Similarity 51.3%; Pred. No. 1.2e-06;
Matches 155; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 532 TATGACAGAGACATGAGAAATATGAAGAGCTGTTGGGCTACCAAGACTCTTGT 591
Db 226 TATGGGCAAAAGAAATGGCTGATTAATCAGATGCAAGAAATATCAATAGAACTTACTGT 285

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OY 592 GACCTTACCCAGTGAACCTCAGACATACAGGAACCTTATTACGGAGGAGGAGGCGGC 651
Db 286 GATCTTCTCTGCTGAAAATTCTTGACTACGAAACATCAGTATTATGCAAAAGTTAAGCCATT 345
OY 652 TCGGCTGGAGACTCTCAGATGAGATGAGCATGACGCGGGTTCACCTCCCTG67GGAAACA 711
Db 346 TGGGGAACAAGATGTTTCCAAATGAGGCTGAAAGTGGAGGTTCTATCTTTTAAACAACA 405
OY 712 AAAATGATCCTCCATGCATGATATATTAACCAAGTCAATGGCTCTTGTGTAATCTC 771
Db 406 CAAATTTGGCCCAACGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGCTCG 465
OY 772 CATGCTCCAAATTTACATATAGATATACCAAAAGAAAAAATGATCTATAGAGATTAC 831
Db 466 ACACCTCCAGAGAAAGTGAGAGAGAAATCCAGAAAGCTTCTCTGTTCCATCCAAACAATC 525
OY 832 TA 833
526 TA 527

RESULT 13
US-08-943-087-21
; Sequence 21, Application US/08943087
; Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1659
OTHER INFORMATION:

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US-08-943-087-21
Query Match          5.0%: Score 66.4; DB 2: Length 1659;
Best Local Similarity 51.3%: Pred. No. 14e-06;
Matches 154; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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QY 568 TTGTACTTACCTAGCACTGAAACCTCAGACATACAGAACTTATTACGGAGGCTAGGGC 647
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DB 282 CTGTATCTTTCTTGTGTGAACCTCTGACTACGACACAGATATATGCCAAAGTTAAGGC 341

QY 648 GGCCTCGCTGGAGACTCTACTCAGATGAGACGCGCGGTTCACTCCCTGTGTGGA 707
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DB 342 CATTTGGGGCAAAAGTGTTCCAAAATGGGCTCAAAAGTGGCGGTTTATCTTTTATGA 401

QY 708 AACAAATAGATCTCTCCAGTCATGATATATACCAAGTCATGGCTCTTTGTGGTAT 767
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 402 AACACAAATTTGGCCCAACGAGAGTGGCACTGACTACAGATGAGAAATGCATTTGTGT 461

QY 768 TCTCATGCTCCAAATTATTCATATATACATACAAAGGAAAAATGTATCTATAGACA 827
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DB 462 CCTGACAGCTCCAGAGAAAGTGAAGGAATCCAGAAAGACTTCTCTTTTCATGCAACA 521

RESULT 14
US-08-943-087-57
: Sequence 57, Application US/08943087
: Patent No. 5945511
: GENERAL INFORMATION:
:   APPLICANT: Lok, Si
:   APPLICANT: Kho, Choon J.
:   APPLICANT: Jelmberg, Anna C.
:   APPLICANT: Adams, Robyn L.
:   APPLICANT: Whitmore, Theodore E.
:   APPLICANT: Farrah, Theresa M.
:   TITLE OF INVENTION: CYTOKINE RECEPTOR
:   NUMBER OF SEQUENCES: 60
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Zymogenetics, Inc.
:   STREET: 1201 Eastlake Avenue East
:   CITY: Seattle
:   STATE: WA
:   COUNTRY: USA
:   ZIP: 98102
:   COMPUTER READABLE FORM:
:   MEDIUM TYPE: Diskette
:   COMPUTER: IBM Compatible
:   OPERATING SYSTEM: DOS
:   SOFTWARE: FASTSEQ for Windows Version 2.0
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/943,087
:   FILING DATE:
:   CLASSIFICATION: 536
:   PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: 08/803,305
:   FILING DATE: 20-FEB-1997
:   ATTORNEY/AGENT INFORMATION:
:   NAME: Lunn, Paul G
:   REGISTRATION NUMBER: 32,743
:   REFERENCE/DOCKET NUMBER: 96-24C1
:   TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 206-442-6627
:   TELEFAX: 206-442-6678
:   TELLEX:
:   INFORMATION FOR SEQ. ID NO: 57:
:   SEQUENCE CHARACTERISTICS:
:   LENGTH: 663 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear

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MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...663
OTHER INFORMATION:
US-08-943-087-57

Query Match
Best Local Similarity 51.2%; Score 65.4; DB 2; Length 663;
Pred. No. 1.9e-06;
Matches 153; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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QY 589 TGTGACCTTACCACTGAAACCTCAGACATACAGGAACCTATTATCGGAGGAGGTAGGGCG 648
DB 196 TGTGATCTTTCTGCTGACACTTCTGACTACGACACCAAGTATATGCAAGTTAAAGGCC 255
649 GCCTGGCTGGGAGCTACTCAGATGAGCAGTACGCGCGGCTTCACTCCCTGGTGGAA 708
256 ATTTGGGGAACAAGTGTCCAAATGCGCTGACAGTGGAGGTTCTATCCTTTTGTAGAC 315
QY 709 ACAAAATAGATCTCTCCAGTCAATGATATATACCCAGTCAATGGCTTTGTGTGTAATT 768
DB 316 ACACAATTTGGCCCAACAGAGTGGCAGTCTGACTACAGATGAGAAGTCCATTTCTGTGTC 375
QY 769 CTCATGCTCCAAATTTACATATAGATACCAAAAGAAAAAATATATATAGAAAGA 827
DB 376 CTGACAGCTCCAGAGAAGTGAAGAAGAAATCCAGAGACCTTCTCTTTCATGACACA 434

RESULT 15

US-08-943-087-29
Sequence 29, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:

APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1659
OTHER INFORMATION:
US-08-943-087-29

Query Match
Best Local Similarity 51.2%; Score 65.4; DB 2; Length 1659;
Pred. No. 2.5e-06;
Matches 153; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

QY 529 AATATGGACAGACAGCAATGAAAAATTAAGAAGACTGTGGGGTACTCAGAACTCTCT 588
DB 223 ATATATGGGCAAGAAAGAGTGTGAATTAATGTCAGAAATGCAAAATATCAATAGAACCTAC 282
QY 589 TGTGACCTTACCACTGAAACCTCAGACATACAGGAACCTTATTAGGGAGGTAGGGCG 648
DB 283 TGTGATCTTTCTGCTGAAACTTCTGACTACGACACCACTATTTATGCCAAGTTAAAGGCC 342
QY 649 GCCTGGCTGGGAGCTACTCAGATGAGCAGTACGCGCGGCTTCACTCCCTGGTGGAA 708
DB 343 ATTTGGGGAACAAGTGTCCAAAGTGGGCTGAAGTGGACGGTTCATCTTTTGGAA 402
QY 709 ACAAAATAGATCTCTCCAGTCAATGATATATACCCAGTCAATGGCTTTGTGTGTAATT 768
DB 403 ACACAATTTGGCCCAACAGAGTGGCAGTCTGACTACAGATGAGAAGTCCATTTCTGTGTC 462
QY 769 CTCATGCTCCAAATTTACATATAGATACCAAAAGAAAAAATATATATAGAAAGA 827
DB 463 CTGACAGCTCCAGAGAAGTGAAGAAGAAATCCAGAAAGCTTCTCTTTCATGACACA 521

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Job time: 65 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 22, 2002, 08:38:11 ; Search time 63 seconds

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Title: US-09-964-994-1

Perfect score: 1318

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Scoring table: IDENTITY_NUC

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Searched: 356696 seqs, 198428768 residues

1 number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:*

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	171.4	13.0	478	10	US-09-864-761-15058
5	171.4	13.0	528	10	US-09-864-761-6687
6	170	12.9	170	10	US-09-864-761-23421
7	128	9.7	128	10	US-09-864-761-31588
8	75.4	5.7	1806	10	US-09-746-359A-36
9	69.2	5.3	424	10	US-09-746-359A-10
10	67	5.1	1720	10	US-09-746-359A-52
11	67	5.1	1750	12	US-10-052-586-397
12	67	5.1	1801	10	US-09-746-359A-22
13	67	5.1	3516	10	US-09-746-359A-10
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15	64.2	4.8	337	10	US-09-960-352-8533
16	63	4.7	447	10	US-09-960-352-8533
17	62.2	4.7	308	10	US-09-960-352-12673
18	61.4	4.7	277	10	US-09-960-352-12673
19	61.4	4.7	1492	10	US-09-925-299-112

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	22	60.4	4.6	3772	9	US-09-989-293A-61	Sequence 61, Appl
	23	60.4	4.6	3772	10	US-09-989-722-61	Sequence 61, Appl
	24	60.4	4.6	3772	10	US-09-989-722-61	Sequence 61, Appl
	25	60.4	4.6	3772	10	US-09-989-722-61	Sequence 61, Appl
	26	60.4	4.6	3772	10	US-09-989-722-61	Sequence 61, Appl
	27	60.4	4.6	3772	10	US-09-989-722-61	Sequence 61, Appl
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	36	60.2	4.6	415	10	US-09-960-352-13784	Sequence 61, Appl
	37	59.6	4.5	239	10	US-09-960-352-6669	Sequence 61, Appl
	38	59.6	4.5	312	10	US-09-960-352-11438	Sequence 61, Appl
	39	59	4.5	312	10	US-09-960-352-8414	Sequence 6869, Ap
	40	58.8	4.5	347	10	US-09-960-352-3371	Sequence 8414, Ap
	41	58.6	4.4	302	10	US-09-925-299-710	Sequence 3371, Ap
	42	58.4	4.4	419	10	US-09-960-352-11234	Sequence 710, App
	43	58.4	4.4	236	10	US-09-960-352-12183	Sequence 11234, A
	44	58.4	4.4	298	10	US-09-960-352-1004	Sequence 1004, Ap
	45	58.2	4.4	325	10	US-09-764-846-30	Sequence 30, Appl
						US-09-764-846-105	Sequence 105, Appl

ALIGNMENTS

RESULT 1
US-09-964-994-1
Sequence 1, Application US/09964994
Patent No. US20020137909A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING SEQUENCE SIMILARITY TO
FILE REFERENCE: P312R1
CURRENT APPLICATION NUMBER: US/09/964,994
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US 60/191,015
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/941,992
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
LENGTH: 1318
TYPE: DNA
ORGANISM: Homo Sapien
US-09-964-994-1

Query Match 100.0%; Score 1318; DB 10; Length 1318;
Best Local Similarity 100.0%; Pred. No. 6.5e-254;
Matches 1318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CAGTTCTTCATCTGTAACATCAATGATATATATATACCAATCTCTAGACTTATAGA 60
QY 61 GGATTACAAAGACAAATATGGAAGAAACATATACATGGCTCCATATATATGATCT 120
DB 61 GGATTACAAAGACAAATATGGAAGAAACATATACATGGCTCCATATATATGATCT 120

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121 TATTATTGACACTAAATGCAATTAATAATTAACAAAGAGAGACAGCATCTGTTCTCT 180
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181 TTGGTCTGAGCTGTTAAAGAGAACTGTTGCCGTGACAGTCACTTGTGACCAATG 240
241 ATGCTTAACATGCTGTTCTGAGCTTCCCTCATGTTCTTCTTCTTCTGAGCAGCA 300
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421 GTGAGTACAAATCATGTTCTCATGACATGAAAGCTCTCAGCAGAAAGCAAGTGA 480
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481 TCGTGGCAGACATTTCTTGTAACTTCCAGGCTGCAAGCAATTTGCTAATTTT 540
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1261 GAGAAATAGTGTCTATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1318

RESULT 2
US-09-728-911-1
; Sequence 1, Application US/09728911
; Patient No. US2002012699A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-93
; CURRENT APPLICATION NUMBER: US/09/728,911
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/169,049
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/232,219
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/244,610
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2149
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(693)
; US-09-728-911-1

Query Match 63.1%; Score 831.6; DB 10; Length 2149;
Best Local Similarity 90.4%; Pred. No. 5.8e-157;
Matches 951; Conservative 0; Mismatches 4; Indels 97; Gaps 2;

QY 238 ATGATGCTTAACATTTGCTTCTGAGCTTCTCATATGATTTCTTCTTCTTCTGATGCA 297
DB 1 ATGATGCTTAACATTTGCTTCTGAGCTTCTCATATGATTTCTTCTTCTTCTGATGCA 60
QY 298 GGAATCTCAACGATGAGTCTGGAAGCCTCAGAGGTAACAATTTCTGCTCCGAAT 357
DB 61 GGAATCTCAACGATGAGTCTGGAAGCCTCAGAGGTAACAATTTCTGCTCCGAAT 120
QY 358 TTTCACAACTTTTGCATGCGAGCTGGAGAGGCACTTACTGCAACAGCAGTGTAT 417
DB 121 TTTCACAACTTTTGCATGCGAGCTGGAGAGGCACTTACTGCAACAGCAGTGTAT 180
QY 418 TTGTGCACTACAAATCATGTTCTCATGAGCATGAAAAAGCTCTCAGCAAGGCCAAGT 477
DB 181 TTGTGCACTACAAATCATGTTCTCATGAGCATGAAAAAGCTCTCAGCAAGGCCAAGT 197
QY 478 GGATGCTGGCAGACATTTCTTGAATTTCCAGAGCTGAGAACATTTGCTTAATATGGA 537
DB 198 -----ATATGA 204
QY 538 CAGAGCAATGGAATAAATAAGAGAGCTGTTGGGTAAGTCAAGAACTCTTGTGACCTT 597
DB 205 CAGAGCAATGGAATAAATAAGAGAGCTGTTGGGTAAGTCAAGAACTCTTGTGACCTT 264
QY 598 ACCAGTGAACCTCAGACATACAGAACTTATTTAGCGGAGGAGGAGGCGGCTCGGCT 657
DB 265 ACCAGTGAACCTCAGACATACAGAACTTATTTAGCGGAGGAGGAGGCGGCTCGGCT 324
QY 658 GGGAGTACTCAGAAATGAGAGATGAGCGCGGTTCACTCCCTGTTGGGAAACAAAAATA 717
DB 325 GGGAGTACTCAGAAATGAGAGATGAGCGCGGTTCACTCCCTGTTGGGAAACAAAAATA 384

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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: This degenerate nucleotide sequence encodes the
OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
NAME/KEY: misc_feature
LOCATION: (1)...(693)
OTHER INFORMATION: n = A,T,C or G

```

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; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

```

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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 15058
LENGTH: 478
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL050337.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
US-09-864-761-15058

Query Match      13.0%  Score 171.4;  DB 10;  Length 478;
Best Local Similarity 99.4%  Pred. No. 1.2e-25;
Matches 172;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0.

QY  708  AACAAATAGTCTCTCCAGTCATATATATACCAAGTCATGCTCTTGTGTAAT 767
Db  475  AGCAAAATAGTCTCTCCAGTCATATATATACCAAGTCATGCTCTTGTGTAAT 416
QY  768  TCTCATCTCTCCAAATTTACCATATAGATACCAAGGAAAAAATGATCTATAGAGA 827
Db  415  TCTCATCTCTCCAAATTTACCATATAGATACCAAGGAAAAAATGATCTATAGAGA 356
QY  828  TTACATGACACTACTATACCGAGTTTATATTAATTAACATTCATCGAAGAAG 880
Db  355  TTACATGACACTACTATACCGAGTTTATATTAATTAACATTCATCGAAGAAG 303

RESULT 5
US-09-864-761-6687
; Sequence 6687, Application US/09864761
; Patent No. US20020048763A1

```

```

GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USED
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 6687
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL158138.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
US-09-864-761-6687

Query Match      13.0%; Score 171.4; DB 10; Length 528;
Best Local Similarity 99.4%; Pred. No. 1.3e-25;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY       708 AACAAATAAGTCCGTCAGTCATCATATATAACCAAGTCAATGGCTCTTTGTGTAT 767
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        176 AGCAAAATAGACTCCAGTCATGAATAATACCACAAGTCATGGCTCTTTGTGTAT 235
QY       768 TCTGCATGCTCCAATTATTAACCATATATACCAAAAAGAAAAATGATCTATAGAGA 827

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|||||
Db 236 TCTCATGCTCCAAATTACCATATAGATACCAAGAAAAAATGTCTATACAAAG 295
QY 828 TTACTATGACTACTATACCGAGTTTATATATTAATTAACATTACTAGAAAG 880
|||||
Db 296 TTACTATGACTACTATACCGAGTTTATATTAATTAACATTACTAGAAAG 348
|||||
RESULT 6
US-09-864-761-23421
; Sequence 23421, 'Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23421
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL158138.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EST_HUMAN HIT: AV714177.1, EVALU 2.00e-78
; OTHER INFORMATION: SWISSPROT HIT: O28438, EVALU 1.30e+00
US-09-864-761-23421
Query Match 12.9%; Score 170; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 710 CAAAAATAGATCCCTCCGATGATATATTAACCCCAAGTCATGCTCTTTGGTAATTC 769
Db 1 CAAAAATAGATCCCTCCGATGATATATTAACCCCAAGTCATGCTCTTTGGTAATTC 60
QY 770 TCCATGCTCCAAATTTACCATATAGATACCAAGAAAAAATGTATCTATAGAGATT 829
Db 61 TCCATGCTCCAAATTTACCATATAGATACCAAGAAAAAATGTATCTATAGAGATT 120
QY 830 ACTATGACTACTATACCGAGTTTATTAATTAACATTACTAGAAAG 879
Db 121 ACTATGACTACTATACCGAGTTTATTAATTAACATTACTAGAAAG 170
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RESULT 7
US-09-864-761-31588/c
; Sequence 31588, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117

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SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SPO ID NO 31588
LENGTH: 128
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL050337.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
OTHER INFORMATION: EST HUMAN HIT: AV714177.1, EVALUE 1.00e-53
OTHER INFORMATION: SWISSPROT HIT: O28438, EVALUE 1.80e+00
US-09-864-761-31588

Query Match
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 710 CAAATAATAGATCTCCAGTCATGATATATTAACCAAGTCAATGGCTCTTTGTGTAATTC 769
128 CAAATAATAGATCTCCAGTCATGATATATTAACCAAGTCAATGGCTCTTTGTGTAATTC 69
770 TCCATGCTCCAAATTTACCATATAGATACCAAAAGAAAAAATGTATATAGAGATT 829
68 TCCATGCTCCAAATTTACCATATAGATACCAAAAGAAAAAATGTATATAGAGATT 9
Db 830 ACTATGAA 837
8 ACTATGAA 1

RESULT 8
US-09-746-359A-36
Sequence 36, Application US/09746359A
Patent No. US20020042366A1
GENERAL INFORMATION:
APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenfeng
APPLICANT: Madden, Karen L.
APPLICANT: Kelly, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
APPLICANT: Eagan, Maribeth A.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekhar, Yasmin A.
APPLICANT: No. US20020042366A1ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 1806
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (38)...(1675)
US-09-746-359A-36

Query Match
Best Local Similarity 5.7%; Score 75.4; DB 10; Length 1806;
Matches 214; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

OY 383 CTGGAGGAGGCACTTACTGACACAGCACTGCTATTTGTGAGTACAAATATCATGTTCT 442
123 CGGGACGGCAGTTCCTGTGTCTGTGTGTCTTAACCTCAAAATATACCTTCT 182
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OY 443 CATGCACATGAANAAGCTCTCACAGAACCCAGTGGATGCTGGAGCAGCAATTTCTTCTGA 502
183 TATCCATCAACATGAGAAATGCTGCTGCAATTCACCGAGAGTGTACAGGAGTTG 242
OY 503 ACTTCCAGGCTGCAGAACTGCTTAATATGAGACAGACAAATGAATAAAG 562
243 AAGTCACATACAGTGTGCAATATTTATATATGAGACAGAAATGCTGATGCTCTGA 302
OY 563 ACTGTGGGTACTACAAAGACTCTTGTGACCTTACAGGAAACCTCAGATACAGG 622
303 AATCGGAGAGTATCAAGAGACCTACTGACCTTCTGTTGAGCTCAGACTATGAC 362
OY 623 AACTTATTTAGGAGGAGGTGAGGCGGCTGGAGTCTGAGATGAGACATGA 682
363 ACCAGTTCTATGCCAAAGTGAAGGCAATTTGGAGACCGAGTCTCCAGATGGCGGAGA 422
OY 683 CGCCGGTTCACCTCCCTGTTGGTGGAAACAAATATGATCTCCAGTATATTAACC 742
423 CGGAACGCTTCTATCTCTTCTGTTGAACTCAAGTCAAGCCACAGAGATGGCCGTGACA 482
OY 743 AAGTCATGCTCTTTGTTGTTGTTATTCATGCTCCAAATTTACCATATAGATCCAA 802
483 CTGGGAGAGAGTCAATCTATGCTGCTGACAGCAGCAGAGATGGAAAGAAATTCAC 542
OY 803 AGAAAAAATGTATCTATAGAGA 827
543 AAGACCACTGTTTCTATGACACA 567
Db 543 AAGACCACTGTTTCTATGACACA 567

RESULT 9
US-09-960-352-11218/c
Sequence 11218, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Ningping
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11218
LENGTH: 424
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
US-09-960-352-11218

Query Match
Best Local Similarity 5.3%; Score 69.2; DB 10; Length 424;
Matches 128; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

OY 1093 TGTTTGAGAGATCTTAATAAATGTTTGTATTTCTTAAGCAATATCACTGTA 1152
247 TTTTAAATTTCTTAATAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 188
OY 1153 CACCTTGGGAGCTCTTGTGTTATCCATCTTTATCTTATATTTATTTATTTTATTTT 1212
187 TAAATTTATTTTAAATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 128
OY 1213 TATTTGAGACATTTCCCGCCGAAATTTGAATGTAAGATGAGGAGAGATTAAGTG 1272
127 TTTTATTTTATTTTATTTTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTT 68
OY 1273 TTTTATGAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1318
67 AAAACCAAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 22
Db 67 AAAACCAAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 22

RESULT 10
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US-09-746-359A-52
; Sequence 52, Application US/09746359A
; Patent No. US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenteng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yashmin A.
; APPLICANT: No. US20020042366A1ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 1720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1713)
US-09-746-359A-52

Query Match
Best Local Similarity 5.1%; Score 67; DB 10; Length 1720;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 529 AATATGGACAGAGAAATGAAAGAAATGAAAGACTGTTGGGTACTCAAGACTCTCT 588
Db 208 ATATATGGCAAGAAAGAAATGCTGAATTAATCAAGAAATGCAATATCAATAGAACCTAC 267
Qy 569 TGTGACCTTACCAAGTGAACCTCAGACATACAGAACCTATTACGGAGGAGGAGCGC 648
Db 268 TGTGATCTTTTGTGCGAAGACTTGTGACTACGACACAGATATTATGCCAAGTTAAGGCC 327
Qy 649 GCGTGGCGGCGGAGCTACTCAGATGAGACATGACGCCGCGGTTCACTCCCTGGTGGAA 708
Db 328 ATTTGGGGAACAAAGTGTTCCTCAAAATGGGCTGAAGTGACGGTTTCTATCTTTTGA 387
Qy 709 ACAAAATAGATCTCAGATCATGATATACCAAGTCAATGGCTTTTGTGTAATT 768
Db 388 ACACAAATTTGGCCACGAGAGTGGACACTGACTACAGATGAGAAGTCCATTTCTGTTGC 447
Qy 769 CTCATGCTCCAAATTTACATATAGATACCAAAAGGAAAAAATGATATCTATAGAGA 827
Db 448 CTGACAGCTCCAGAGAAGTGAAGAAATCCAGAAAGACTTCTCTTTCATGACACA 506

RESULT 11
US-10-052-586-397
; Sequence 397, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
```

```
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
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Best Local Similarity 51.5%; Pred. No. 0.00011;
Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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QY 589 TGTGACCTTACCACTGAAACCTCAGCATATACGAACCTTATACGGAGGCTGAGGCG 648
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DB 311 ATTGGGGAACAAGTGTCCAAATGGCTGAAGAGTGACGGTCTTATCTTTTAAAGAA 370
QY 709 AAAAAAATGATCCCTCCACTCATATATACCAAGTAAATGGCTCTTGTGTAATT 768
DB 371 ACACAATTTGGCCACACAGAGTGGCAGCTGACATGAGAGATGAGATTCATTTCTGTGTC 430
QY 769 CTCGATGCTCAAAATTTACATATATGATACCAAAAGAAAAAATGATATAGAGA 827
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RESULT 12
US-09-746-359A-22
Sequence 22, Application US/09746359A
Patent No. US20020042366A1
GENERAL INFORMATION:

APPLICANT: Thompson, Penny
 APPLICANT: Foster, Donald C.
 APPLICANT: Xu, Wenfeng
 APPLICANT: Madden, Karen L.
 APPLICANT: Kelly, James D.
 APPLICANT: Sprecher, Cindy A.
 APPLICANT: Blumberg, Hal
 APPLICANT: Eagan, Maribeth A.
 APPLICANT: Jaspers, Stephen R.
 APPLICANT: Chandrasekhar, Yashmin A.
 APPLICANT: No. US20020042366A1ak, Julia E.
 TITLE OF INVENTION: Method for Treating Inflammation
 FILE REFERENCE: 99-108
 CURRENT APPLICATION NUMBER: US/09/746,359A
 PRIOR FILING DATE: 2001-05-21
 PRIOR APPLICATION NUMBER: 60/171,969
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 60/213,341
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: FastSeq for Windows Version 3.0
 US-09-746-359A-22

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 Best Local Similarity 51.5%; Pred. No. 0.00011;
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 589 TGTGACCTTACCAAGTGAACCTGACATGACAGAACTTATTACGGAGGGTGGGCG 648
 308 TGTGACCTTACCAAGTGAACCTGACATGACAGAACTTATTACGGAGGGTGGGCG 367
 649 GCCTGGCTGGGAGCTACTGACATGACAGAACTTATTACGGAGGGTGGGCG 708
 368 ATTTGGGGAACAAGTGTTCCTCAATATGCGCTGAAGTGGAGCGTTTATCTTTTGA 427
 709 ACAAAATAGATCTCCAGCTGATGATATACCAAGTCAATGCTTTTGTGTAATT 768
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RESULT 13
 US-09-746-359A-10
 Sequence 10, Application US/09746359A
 Patent No. US20020042366A1
 GENERAL INFORMATION:
 APPLICANT: Thompson, Penny
 APPLICANT: Foster, Donald C.
 APPLICANT: Xu, Wenfeng
 APPLICANT: Madden, Karen L.
 APPLICANT: Kelly, James D.
 APPLICANT: Sprecher, Cindy A.
 APPLICANT: Blumberg, Hal
 APPLICANT: Eagan, Maribeth A.
 APPLICANT: Jaspers, Stephen R.
 APPLICANT: Chandrasekhar, Yashmin A.
 APPLICANT: No. US20020042366A1ak, Julia E.
 TITLE OF INVENTION: Method for Treating Inflammation
 FILE REFERENCE: 99-108

CURRENT APPLICATION NUMBER: US/09/746,359A
 CURRENT FILING DATE: 2001-05-21
 PRIOR APPLICATION NUMBER: 60/171,969
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 60/213,341
 PRIOR FILING DATE: 2000-06-22
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 10
 LENGTH: 3516
 TYPE: DNA
 ORGANISM: Homo sapiens
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 NAME/KEY: CDS
 LOCATION: (237)...(1895)
 US-09-746-359A-10

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 Matches 154; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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 649 GCCTGGCTGGGAGCTACTGACATGACAGAACTTATTACGGAGGGTGGGCG 708
 579 ATTTGGGGAACAAGTGTTCCTCAATATGCGCTGAAGTGGAGCGTTTATCTTTTGA 638
 709 ACAAAATAGATCTCCAGCTGATGATATACCAAGTCAATGCTTTTGTGTAATT 768
 639 ACACAAATTTGGCCACACAGAGTGGCAGCTACAGATGAGAGTCCATTCTGTTGTC 698
 769 CTCATGCTCCAAATTTTACATATGATACCAAAAGGAAAAAATATCTATCTATAGA 827
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RESULT 14
 US-09-960-352-12673/c
 Sequence 12673, Application US/09960352
 Patent No. US20020137139A1
 GENERAL INFORMATION:
 APPLICANT: Warren, Wesley C.
 APPLICANT: Tao, Nengbing
 APPLICANT: Byatt, John C.
 APPLICANT: Mathialagan, Nagappan
 TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 FILE REFERENCE: 16511.006/37-21(10298)C
 CURRENT APPLICATION NUMBER: US/09/960,352
 CURRENT FILING DATE: 2001-09-24
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Query Match
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1080 ACAGAGAGCTGTTGTAAGATCTTAAATGTTTGTGTTTCTTAAAGCA 1139
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 1140 AATATGACAGCTTACAGCTTGGGAGCTTCTTGTATTCATCTTTATCTTATATT 1199

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OM protein - protein search, using sw model

Run on: December 22, 2002, 09:11:22 ; Search time 67 seconds

(without alignments)
521.070 Million cell updates/sec

Title: us-09-964-994-2

Perfect score: 1427
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1427	100.0	262	22	AAU09186
2	1427	100.0	263	23	AAE17321
3	1423	99.7	263	23	AAO17382
4	1392	97.5	263	23	AAU80324
5	1213	85.0	231	22	AAE05048
6	1213	85.0	231	22	AAE02460
7	1213	85.0	231	22	AAE62657
8	1213	85.0	231	23	AAO17381
9	1213	85.0	231	23	AAU80000
10	1213	85.0	231	23	ABG34086

11	1213	85.0	231	23	AAE17320	Human cytokine rec
12	1114	78.1	214	22	AAE17319	Human cytokine rec
13	1104	77.4	210	22	AAE62663	Human zcyto16 ext
14	1045	73.2	249	22	AAE02458	Human DNAX cytokin
15	1045	73.2	249	22	AAO17380	Human cytokine rec
16	656	46.0	130	22	AAE02461	Human DNAX cytokin
17	310	21.7	207	22	AAE85289	Human IL-20 recept
18	310	21.7	207	22	AAE67220	Interleukin-20 sub
19	310	21.7	214	22	AAE85287	Interleukin-20 sub
20	310	21.7	214	22	AAE67218	Human IL-20 recept
21	310	21.7	217	23	AAE85280	Interleukin-20 sub
22	310	21.7	217	23	AAE67211	IL-20RA-Ig gamma1
23	310	21.7	221	23	AAE85269	Interleukin-20 sub
24	310	21.7	221	23	AAE67200	Human IL-20 recept
25	310	21.7	221	23	AAE23354	Human Interleukin-
26	310	21.7	542	22	AAE29222	Human IL-20RA matu
27	310	21.7	542	22	AAU12265	Human PRO polypt
28	310	21.7	547	22	AAE85279	Human PRO4978 poly
29	310	21.7	547	23	ABG67210	Human IL-20RA-Ig g
30	310	21.7	547	23	AAE23362	Human IL-20RA/I
31	310	21.7	553	19	AAE79159	Human IL-20RA EC d
32	310	21.7	553	22	ABE11582	Human class II cyt
33	310	21.7	553	22	AAU04058	Human Interleukin-
34	310	21.7	553	22	AAE85268	Human IL-20 recept
35	310	21.7	553	23	ABG67199	Human Interleukin-
36	310	21.7	553	23	AAE23353	Human Interleukin-
37	310	21.7	555	22	AAU04072	Human IL-20RA/I
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39	310	21.7	559	22	AAE67217	Human IL-20RA/I
40	310	21.7	559	23	AAE23361	Human IL-20RA EC d
41	310	21.7	571	22	AAU04065	Human IL-20RA/I
42	310	21.7	571	22	AAE85278	Human IL-20RA/I
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44	310	21.7	571	23	AAE23359	Human IL-20RA ext
45	310	21.7	594	22	AAU04062	Human IL-20RA/I

ALIGNMENTS

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ID AAU09186 standard; Protein; 262 AA.
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AC AAU09186;
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DT 16-JAN-2002 (first entry)
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DE Human PRO19598 polypeptide.
XX
KW Human: PRO19598; clone DMA145887; immune-related disorder;
KW inflammatory disorder; infectious disorder; immunodeficiency disorder;
KW autoimmune disorder; renal disease; demyelinating disease; skin disease;
KW neoplasia; transplantation associated disease; immunosuppressive;
KW anti-inflammatory; antidiabetic; antidiabetic.
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OS Homo sapiens.
XX
FH Key
FH Peptide
FT 1..20 Location/Qualifiers
FT 17..22 /label= "Signal_peptide"
FT Modified-site
FT /note= "N-myristoylation site"
FT 20..25 /note= "N-myristoylation site"
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FT 55..58 /note= "N-glycosylation site"
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FT 165..168 /note= "N-glycosylation site"
FT Modified-site
FT 170..173 /note= "N-glycosylation site"
FT Modified-site
FT /note= "N-glycosylation site"

CC allergies, schizophrenia, sbg442445PROA-associated disorders,
 CC septicolaemia, psoriasis, inflammatory bowel disease, transplant rejection,
 CC graft versus host disease, ischaemia, stroke, acute respiratory disease
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
 CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
 CC depression, anxiety disorders and sleep disorders, cardiovascular
 CC diseases including congestive heart failure and myocardial infarction,
 CC respiratory diseases including chronic obstructive pulmonary disease,
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders
 CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
 CC and tendinitis, gastrointestinal diseases including intestinal
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
 CC reproductive diseases including low testosterone and male infertility.
 CC The present sequence is human cytokine receptor.

XX Sequence 263 AA:

Query Match 100.0%; Score 1427; DB 23; Length 263;
 Best Local Similarity 100.0%; Pred. No. 2, 4e-134;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPKHCFGLISFLFTGAGTOSTHESLKPQVQFOSRNFHNILOMPGRALTGNSVYF 60
 DB 2 MPKHCFGLISFLFTGAGTOSTHESLKPQVQFOSRNFHNILOMPGRALTGNSVYF 61
 QY 61 VQKIMFSCSKSSHQPSGCWQHISCNFPGCRTLAKYGGOROMKNEKDCWGTOLSCDLT 120
 DB 62 VQKIMFSCSKSSHQPSGCWQHISCNFPGCRTLAKYGGOROMKNEKDCWGTOLSCDLT 121
 QY 121 SETSDIOEPYGRVRAASAGSYSMSMTPRFTPWETKIDPPVNNITQVNGSLVILHAP 180
 DB 122 SETSDIOEPYGRVRAASAGSYSMSMTPRFTPWETKIDPPVNNITQVNGSLVILHAP 181
 QY 181 NLPRYQKEKNVSIEDYELLRYFIIINNSLEKEQKYEGAHRAVEIALTPHSSYCVA 240
 DB 182 NLPRYQKEKNVSIEDYELLRYFIIINNSLEKEQKYEGAHRAVEIALTPHSSYCVA 241
 QY 241 EIIQPMIDRRSRSEERCVEIP 262
 DB 242 EIIQPMIDRRSRSEERCVEIP 263

RESULT 3
 AA017382

AA017382 standard; Protein; 263 AA.

AC AA017382;

DT 08-AUG-2002 (first entry)

DE Human cytokine receptor variant 3.

XX Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
 KW Rheumatoid arthritis; multiple sclerosis; Crohn's disease;
 KW ulcerative colitis; transplant rejection; abortion; antiproliferative;
 KW immunosuppressive; antineuritic; antitubercular; neuroprotective;
 KW antiinflammatory; antitubercular; cytoskeletal; dermatological;
 KW chromosome 6q24.1-25.2; receptor.

OS Homo sapiens.

XX EP1191035-A2.

XX 27-MAR-2002.

XX 24-AUG-2001; 2001EP-0250307.

XX 25-SEP-2000; 2000DE-1048626.

XX 17-NOV-2000; 2000DE-1058907.

PR 19-DEC-2000; 2000DE-1064906.

XX (SCHD) SCHERING AG.

XX Weiss B, Sabat R, Assadullah K, Toshi L;

XX WPI: 2002-332210/37.

DR N-PSDB; AAL46001.

PT New nucleic acid encoding soluble cytokine receptor, useful for

PT diagnosis and treatment of e.g. immune disease, also related protein

PS Claim 6; Page 15; 21pp; German.

CC The present invention provides the protein and coding sequences of 3
 CC variants of a human cytokine receptor. The sequences can be used in the
 CC diagnosis, prevention and treatment of immune diseases, including
 CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
 CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
 CC transplant rejection and in reproductive medicine, e.g. for diagnosing
 CC abnormal immune reactions which cause abortions. The present sequence is
 CC variant 3 of the invention.

XX Sequence 263 AA:

Query Match 99.7%; Score 1423; DB 23; Length 263;
 Best Local Similarity 99.6%; Pred. No. 6e-134;
 Matches 261; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPKHCFGLISFLFTGAGTOSTHESLKPQVQFOSRNFHNILOMPGRALTGNSVYF 60
 DB 2 MPKHCFGLISFLFTGAGTOSTHESLKPQVQFOSRNFHNILOMPGRALTGNSVYF 61
 QY 61 VQKIMFSCSKSSHQPSGCWQHISCNFPGCRTLAKYGGOROMKNEKDCWGTOLSCDLT 120
 DB 62 VQKIMFSCSKSSHQPSGCWQHISCNFPGCRTLAKYGGOROMKNEKDCWGTOLSCDLT 121
 QY 121 SETSDIOEPYGRVRAASAGSYSMSMTPRFTPWETKIDPPVNNITQVNGSLVILHAP 180
 DB 122 SETSDIOEPYGRVRAASAGSYSMSMTPRFTPWETKIDPPVNNITQVNGSLVILHAP 181
 QY 181 NLPRYQKEKNVSIEDYELLRYFIIINNSLEKEQKYEGAHRAVEIALTPHSSYCVA 240
 DB 182 NLPRYQKEKNVSIEDYELLRYFIIINNSLEKEQKYEGAHRAVEIALTPHSSYCVA 241
 QY 241 EIIQPMIDRRSRSEERCVEIP 262
 DB 242 EIIQPMIDRRSRSEERCVEIP 263

RESULT 4
 ID AA080324

XX AA080324 standard; Protein; 263 AA.

AC AA080324;

DT 15-JUL-2002 (first entry)

DE Human IL-TIF/IL-22 binding protein #2.

XX Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;

XX IL-TIF/IL-22 antagonist.

OS Homo sapiens.

XX WO200224912-A2.

XX 28-MAR-2002.

XX 21-SEP-2001; 2001WO-US29576.

XX 22-SEP-2000; 2000US-234583P.

PR 03-NOV-2000; 2000US-245495P.
PR 31-JUL-2001; 2001US-091916Z.
XX (LUDM-) LUDMIG INST CANCER RES.
XX Renauld J, Dumoutier L;
XX MPI: 2002-383190/41.
XX N-PSDB; ABR50080.
XX polynucleotide and polypeptide of soluble protein which binds to
PT interleukin-TiF/IL-22 useful for inhibiting effect of IL-TiF/IL-22 on a
PT cell
XX
PS Claim 14; Page 41-42; 42pp; English.
XX
XX The present invention relates to a new polynucleotide that encodes a
CC soluble protein which binds to interleukin (IL)-TiF/IL-22 (also referred
CC to as IL-22BP), where the complementary sequence of the invention
CC hybridizes under stringent conditions to a nucleotide sequence of 2271
or 2366 base pairs, as given in the specification. The molecules of the
CC invention are useful for inhibiting (antagonizing) effect of IL-TiF/IL-22
CC on a cell, for determining whether IL-TiF/IL-22 is present in a sample,
CC for inhibiting binding of IL-TiF/IL-22 to a binding partner, preferably
CC in vitro, and for obtaining an antibody molecule specific for the soluble
CC binding protein of the invention, from a population or panel of antibody
CC molecules of diverse binding specificity. The soluble protein is further
CC useful in manufacture of a medicament for treating an IL-22 mediated
CC disease and for assaying an agent, preferably an antibody or a peptide
CC fragment of IL-TiF/IL-22 or the soluble protein, that modulates binding
CC of the soluble protein to IL-TiF/IL-22, where the agent identified is
CC used in the manufacture of medicament for treating IL-TiF/IL-22 mediated
CC disorder. The antibody is useful for determining presence of the soluble
CC protein. Where the antibody is useful for detectably labelling. The present amino
CC acid sequence represents the human IL-TiF/IL-22 binding protein #2 of
CC the invention.
XX
SQ Sequence 263 AA:
Query Match 97.5%; Score 1392; DB 23; Length 263;
Best Local Similarity 98.1%; Pred. No. 7.6e-131;
Matches 257; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 MPKHCEFLGFLISFELTGVAGTOSTHESLKPQVQFQSRNFHNILOWQGRALTGNSSYF 60
DB 2 MPKHCEFLGFLISFELTGVAGTOSTHESLKPQVQFQSRNFHNILOWQGRALTGNSSYF 61
QY 61 VOYKIMFSCSMKSSHOKPSCGWOHISCNFPGCRTLAKYGQRKKNKEDCGTQELSCDLT 120
DB 62 VOYKIMFSCSMKSSHOKPSCGWOHISCNFPGCRTLAKYGQRKKNKEDCGTQELSCDLT 121
QY 121 SETSDIOEPPYGYGRVRAASAGSYSEMSMTPTPTPMWETKIDPPVANNITQVNGSLVLIHAP 180
DB 122 SETSDIOEPPYGYGRVRAASAGSYSEMSMTPTPTPMWETKIDPPVANNITQVNGSLVLIHAP 181
QY 181 NLPYRQKEKNVSIEDYELLVRFVFIINNSLEKEQKYEGAHRAVEIALTPHSSYCYVA 240
DB 182 NLPYRQKEKNVSIEDYELLVRFVFIINNSLEKEQKYEGAHRAVEIALTPHSSYCYVA 241
QY 241 ETYQPMIDRRSQSRSERCVEIP 262
DB 242 ETYQPMIDRRSQSRSERCVEIP 263

XX
KW Human: cytosolic; cytokine; ZCYTO18 protein; genetic abnormality;
KW cancer; inflammation; gene therapy; zcytor16.
XX
XX Homo sapiens.
XX WO200146422-A1.
XX
XX 28-JUN-2001.
XX
XX 22-DEC-2000; 2000WO-US35308.
XX
XX 23-DEC-1999; 99US-0471767.
XX 01-DEC-2000; 2000US-0250841.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Presnell SR, Kindsvogel W;
XX MPI: 2001-408648/43.
XX N-PSDB; AAD09745.
XX
XX Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX Example 13A; Page 158-159; 167pp; English.
XX
XX The patent discloses novel human cytokine, ZCYTO18 protein and its
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC expressing ZCYTO18, a receptor for ZCYTO18 or induces cytotoxicity
CC in K562 cells. ZCYTO18 DNA is useful for detecting a genetic
CC abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
CC for detecting cancer and inflammation. ZCYTO18 protein is useful for
CC killing cancer cells. It is useful for increasing platelets in a
CC patient or injured tissue. It is also used in gene therapy.
CC The present sequence is human zcytor16, which is a naturally expressed
CC soluble receptor antagonist of ZCYTO18 protein.
XX
SQ Sequence 231 AA:
Query Match 85.0%; Score 1213; DB 22; Length 231;
Best Local Similarity 87.8%; Pred. No. 5.2e-113;
Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
QY 1 MPKHCEFLGFLISFELTGVAGTOSTHESLKPQVQFQSRNFHNILOWQGRALTGNSSYF 60
DB 2 MPKHCEFLGFLISFELTGVAGTOSTHESLKPQVQFQSRNFHNILOWQGRALTGNSSYF 61
QY 61 VOYKIMFSCSMKSSHOKPSCGWOHISCNFPGCRTLAKYGQRKKNKEDCGTQELSCDLT 120
DB 62 VOYKIMFSCSMKSSHOKPSCGWOHISCNFPGCRTLAKYGQRKKNKEDCGTQELSCDLT 89
QY 121 SETSDIOEPPYGYGRVRAASAGSYSEMSMTPTPTPMWETKIDPPVANNITQVNGSLVLIHAP 180
DB 90 SETSDIOEPPYGYGRVRAASAGSYSEMSMTPTPTPMWETKIDPPVANNITQVNGSLVLIHAP 149
QY 181 NLPYRQKEKNVSIEDYELLVRFVFIINNSLEKEQKYEGAHRAVEIALTPHSSYCYVA 240
DB 150 NLPYRQKEKNVSIEDYELLVRFVFIINNSLEKEQKYEGAHRAVEIALTPHSSYCYVA 209
QY 241 ETYQPMIDRRSQSRSERCVEIP 262
DB 210 ETYQPMIDRRSQSRSERCVEIP 231

XX Human: immunomodulator; DNAX cytokine receptor subunit 4.2; DCRS4.2;
 KW therapy; immunological disorder; drug screening; cell development;
 KM chromosome 6q24.1-25.2.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label= Signal-peptide
 FT 22..231
 FT /label= DCRS4.2
 FT /note= "Human mature DNAX cytokine receptor
 subunit 4.2"

XX WO200136467-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000WO-US31363.

XX 18-NOV-1999; 99US-0443060.
 PR 13-DEC-1999; 99US-0170320.
 XX

XX (SCHE) SCHERING CORP.

XX Gorman DM;
 PI
 DR MPI; 2001-343800/36.
 DR N-PSDB; AAD06414.
 XX

XX New mammalian receptor proteins related to cytokine receptors, useful
 PT for regulating cell development and for diagnosis and treatment of
 PT immunological disorders
 XX

XX Claim 3; Page 23; 124pp; English.

XX The present sequence is human DNAX cytokine receptor subunit 4.2
 CC (DCRS4.2). DCRS4 gene is located on chromosome 6q24.1-25.2.
 CC Cytokine receptors, fragments and antibodies are useful for treating
 CC immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
 CC useful in drug screening to identify compounds having binding affinity
 CC to the receptor subunit. Modulators of DCRS are useful for modulating
 CC the physiology or development of a cell or tissue culture cells. A
 CC purified DCRS is useful as a reagent to detect antibodies generated in
 CC response to the presence of elevated levels of expression, or
 CC immunological disorders which lead to production of antibody to the
 CC endogenous receptor. Cytokine receptor sequences are useful as probes
 CC for detecting levels of the cytokine receptor in patients suspected of
 CC having an immunological disorder. Antibodies have therapeutic value, are
 CC useful as potent antagonist, in detecting or quantifying ligands, for
 CC isolating DCRS proteins and peptides, to screen expression libraries for
 CC particular expression products, to raise anti-idiotypic antibodies and
 CC for detecting or diagnosing various immunological conditions related to
 CC expression of the protein or cells which express the protein.

XX Sequence 231 AA:
 SQ

XX Query Match 85.0%; Score 1213; DB 22; Length 231;
 XX Best local Similarity 87.8%; Pred. No. 5.2e-113;
 XX Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

XX 1 MKHCHLGLIFLISFTLVAGTOSTHESLKPQVQFOSRNFHNTLQWOPGALNGSSVVF 60
 DB |
 DB 2 MKHCHLGLIFLISFTLVAGTOSTHESLKPQVQFOSRNFHNTLQWOPGALNGSSVVF 61
 DB |
 QY 61 VQYKMFSCSMKSHQKPPSCWQHICNFFGCGTTLAKYGRQKKNKEDCGTDELSDLT 120
 DB |
 DB 62 VQYKTF-----YGRQKKNKEDCGTDELSDLT 89
 DB |
 QY 121 SETSDIQEPIYGVRAASAGSYSEMSMTPTPTPMWETKIDPPVNNITQVNGSLVITIHAP 180
 DB |
 DB 90 SETSDIQEPIYGVRAASAGSYSEMSMTPTPTPMWETKIDPPVNNITQVNGSLVITIHAP 149

QY 181 NLPRYQKEKNWSIEDYYEILYRVFIINNSLEKQKYEAGHRAVETALPHSSCYVA 240
 DB |
 DB 150 NLPRYQKEKNWSIEDYYEILYRVFIINNSLEKQKYEAGHRAVETALPHSSCYVA 209
 DB |
 QY 241 EIQPMLDRSQRSEERCVEIP 262
 DB |
 DB 210 EIQPMLDRSQRSEERCVEIP 231
 DB |

RESULT 7
 ID AAB62657 standard; Protein: 231 AA.
 XX
 AC AAB62657;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Human cytokine receptor, zcytor16.
 XX

XX Cytokine receptor; zcytor16; IL-TiF; antiinflammatory; cytostatic;
 KW antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
 KM immunosuppressive; chromosome 6q24.1-25.2; human.
 XX

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 22..108
 FT /note= "Ig domain 1"
 FT 22..231
 FT Domain
 FT /note= "extracellular domain"
 FT 112..210
 FT /note= "Ig domain 2"
 XX

XX WO200140467-A1.
 XX
 XX 07-JUN-2001.
 XX
 XX 01-DEC-2000; 2000WO-US32703.
 XX
 XX 03-DEC-1999; 99US-0169049.
 PR 13-SEP-2000; 2000US-0232219.
 PR 31-OCT-2000; 2000US-0244610.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
 XX
 DR MPI; 2001-356158/37.
 DR N-PSDB; AAF83735.
 XX

XX New soluble cytokine receptor polypeptides and polynucleotides, useful
 PT for diagnosing and treating cancer and inflammatory conditions
 PT
 XX
 XX Claim 1; Page 186-188; 210pp; English.

XX The invention relates to a human cytokine receptor polypeptide,
 CC designated zcytor16. The zcytor16 polypeptide can be expressed by
 CC standard recombinant methodology and can bind to IL-TiF (undefined). The
 CC zcytor16 protein is useful for: inhibiting IL-TiF induced proliferation
 CC or differentiation of hematopoietic cell(s) (progenitors); reducing
 CC IL-TiF induced or IL-9 induced inflammation; and suppressing an
 CC inflammatory response in a mammal with inflammation. Heteromeric/
 CC multimeric receptor polypeptides such as soluble zcytor 16/CDR2-4 can be
 CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
 CC can also be used to detect IL-TiF levels which is indicative of
 CC pathological conditions including inflammatory states (e.g. rheumatoid
 CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
 CC polypeptides themselves are useful for the treatment of inflammatory,
 CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel
 CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune
 CC diseases. The antibodies and zcytor16 polynucleotides are also useful
 CC for detecting cancer. The present sequence represents the human

CC zcytor16 protein.
 XX Sequence 231 AA:
 SO Query Match 85.0%; Score 1213; DB 22; Length 231;
 Best Local Similarity 87.8%; Pred. No. 5.2e-113;
 Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

1 MKHCFGLGFLISFPLTGVAGTOSTHESLKPQRYOFOSRNFHNLQMPGRLTGNSSYVF 60
 2 MKHCFGLGFLISFPLTGVAGTOSTHESLKPQRYOFOSRNFHNLQMPGRLTGNSSYVF 61
 61 VOYKIMFSCSMKSSHQKPSGCWQHISCNPGCRTLAKYGOORWKNKEDCWGTQELSCDLT 120
 62 VOYKIMFSCSMKSSHQKPSGCWQHISCNPGCRTLAKYGOORWKNKEDCWGTQELSCDLT 89
 121 SETSDIOEPYGRVRAASAGSYSEMSMTPRFTPMWETKIDPPYMNITQVNGSLVILHAP 180
 90 SETSDIOEPYGRVRAASAGSYSEMSMTPRFTPMWETKIDPPYMNITQVNGSLVILHAP 149
 181 NLPYRQKEKNVSIEDYELLRYVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCYVA 240
 150 NLPYRQKEKNVSIEDYELLRYVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCYVA 209
 241 EIIQPMIDRRSQRSEECVEIP 262
 210 EIIQPMIDRRSQRSEECVEIP 231

RESULT 8
 AA017381
 ID AA017381 standard; protein; 231 AA.
 AC AA017381;
 XX 08-AUG-2002 (first entry)
 DE Human cytokine receptor variant 2.
 KW Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
 KW Rheumatoid arthritis; multiple sclerosis; Crohn's disease;
 KW ulcerative colitis; transplant rejection; abortion; antipsoriatic;
 KW immunosuppressive; antiinfective; antiarthritic; neuroprotective;
 KW antiinflammatory; anticancer; cytostatic; dermatological;
 KW chromosome 6q24.1-25.2; receptor.
 XX Homo sapiens.
 OS
 EP1191035-A2.
 PD 27-MAR-2002.
 PF 24-AUG-2001; 2001EP-0250307.
 PR 25-SEP-2000; 2000DE-1048626.
 PR 17-NOV-2000; 2000DE-1058907.
 PR 19-DEC-2000; 2000DE-1064906.
 XX (SCHD) SCHERING AG.
 PA Weiss B, Sabat R, Assadullah K, Tosh I;
 PI WPI: 2002-332210/37.
 DR N-PSDB; AAL46000.
 XX New nucleic acid encoding soluble cytokine receptor, useful for
 PT diagnosis and treatment of e.g. immune disease, also related protein
 PT and antibodies -
 XX Claim 6; Page 14; 21pp; German.
 CC The present invention provides the protein and coding sequences of 3
 CC variants of a human cytokine receptor. The sequences can be used in the

CC diagnosis, prevention and treatment of immune diseases, including
 CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
 CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
 CC transplant rejection and in reproductive medicine, e.g. for diagnosing
 CC abnormal immune reactions which cause abortions. The present sequence is
 CC variant 2 of the invention.
 XX Sequence 231 AA:
 SO Query Match 85.0%; Score 1213; DB 23; Length 231;
 Best Local Similarity 87.8%; Pred. No. 5.2e-113;
 Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

1 MKHCFGLGFLISFPLTGVAGTOSTHESLKPQRYOFOSRNFHNLQMPGRLTGNSSYVF 60
 2 MKHCFGLGFLISFPLTGVAGTOSTHESLKPQRYOFOSRNFHNLQMPGRLTGNSSYVF 61
 61 VOYKIMFSCSMKSSHQKPSGCWQHISCNPGCRTLAKYGOORWKNKEDCWGTQELSCDLT 120
 62 VOYKIMFSCSMKSSHQKPSGCWQHISCNPGCRTLAKYGOORWKNKEDCWGTQELSCDLT 89
 121 SETSDIOEPYGRVRAASAGSYSEMSMTPRFTPMWETKIDPPYMNITQVNGSLVILHAP 180
 90 SETSDIOEPYGRVRAASAGSYSEMSMTPRFTPMWETKIDPPYMNITQVNGSLVILHAP 149
 181 NLPYRQKEKNVSIEDYELLRYVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCYVA 240
 150 NLPYRQKEKNVSIEDYELLRYVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCYVA 209
 241 EIIQPMIDRRSQRSEECVEIP 262
 210 EIIQPMIDRRSQRSEECVEIP 231

RESULT 9
 AA080000
 ID AA080000 standard; protein; 231 AA.
 AC AA080000;
 XX 15-JUL-2002 (first entry)
 DE Human IL-TIF/IL-22 binding protein #1.
 DE Human IL-TIF/IL-22 binding protein #1.
 KW Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
 KW IL-TIF/IL-22 antagonist.
 XX Homo sapiens.
 OS
 WO200224912-A2.
 PD 28-MAR-2002.
 PF 21-SEP-2001; 2001WO-US29576.
 PR 22-SEP-2000; 2000US-234583P.
 PR 03-NOV-2000; 2000US-245495P.
 PR 31-JUL-2001; 2001US-0919162.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Renauld J, Dumoutier L;
 PI WPI: 2002-383190/41.
 DR N-PSDB; ABK50076.
 XX Polynucleotide and polypeptide of soluble protein which binds to
 PT interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
 PT cell -
 XX Claim 14; Page 39; 42pp; English.
 CC The present invention relates to a new polynucleotide that encodes a

CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
CC to as IL-22B), where the complementary sequence of the invention
CC hybridises under stringent conditions to a nucleotide sequence of 2271
CC or 2366 base pairs, as given in the specification. The molecules of the
CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
CC in vitro, and for obtaining an antibody molecule specific for the soluble
CC binding protein of the invention, from a population or panel of antibody
CC molecules of diverse binding specificity. The soluble protein is further
CC useful in manufacture of a medicament for treating an IL-22 mediated
CC disease and for assaying an agent, preferably an antibody or a peptide
CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
CC of the soluble protein to IL-TIF/IL-22, where the agent identified is
CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
CC disorder. The antibody is useful for determining presence of the soluble
CC protein, where the antibody is detectably labelled. The present amino
CC acid sequence represents the human IL-TIF/IL-22 binding protein #1 of
CC the invention.

Sequence 231 AA:

Query Match 85.0%; Score 1213; DB 23; Length 231;

Best Local Similarity 87.8%; Pred. No. 5.2e-113;

Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPKCFGLFLISFPLTGVAGTQSTHESLKPQRYVQFOSRNFNHILOMOPGRALTGSSVYF 60
DB 2 MPKCFGLFLISFPLTGVAGTQSTHESLKPQRYVQFOSRNFNHILOMOPGRALTGSSVYF 61
QY 61 VOYKIMFSCMKSSHQKPSGCMQHOISCFNPGCRITLAKYQGRQWKNKEDCWGTQELSCDIT 120
DB 62 VOYKI-----YGRQWKNKEDCWGTQELSCDIT 89
QY 121 SETSDIOEPYGRVRAASAGSYSEMSMTPTPTPWETKIDPPVNNITQVNSLVLITLAP 180
DB 90 SETSDIOEPYGRVRAASAGSYSEMSMTPTPTPWETKIDPPVNNITQVNSLVLITLAP 149
QY 181 NLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGARRAVEIEALTPHSSVCVYA 240
DB 150 NLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGARRAVEIEALTPHSSVCVYA 209
QY 241 EYQPMIDRSQSRSEECVEIP 262
DB 210 EYQPMIDRSQSRSEECVEIP 231

RESULT 10

ABG34086
ABG34086 standard; Protein; 231 AA.

AC
XX
ABG34086;

DT 15-JUL-2002 (first entry)

DE Human Pro peptide #57.

XX Human; PRO; secreted protein; transmembrane protein;
XX genetic disorder; tumour; cancer.

OS Homo sapiens.

PN WO200224888-A2.

PD 28-MAR-2002.

PF 29-AUG-2001; 2001WO-US277099.

PR 01-SEP-2000; 2000US-229896P.

PR 05-SEP-2000; 2000US-230621P.

PR 22-SEP-2000; 2000US-235147P.

PR 10-NOV-2000; 2000WO-US30873.

PR 12-JAN-2001; 2001US-261878P.

PR 16-JAN-2001; 2001US-261910P.
PR 16-JAN-2001; 2001US-261939P.
PR 16-JAN-2001; 2001US-262150P.
PR 25-JAN-2001; 2001US-264395P.
PR 02-FEB-2001; 2001US-266421P.
PR 09-FEB-2001; 2001US-267623P.
PR 28-FEB-2001; 2001WO-US06520.
PR 09-MAR-2001; 2001US-274399P.
PR 03-APR-2001; 2001US-280982P.
PR 04-APR-2001; 2001US-282129P.
PR 04-APR-2001; 2001US-282199P.
PR 09-MAY-2001; 2001US-290589P.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.

(GETH) GENENTECH INC.

Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,
Fong S;

WPI; 2002-362426/39.
N-PSDB; ABK70017.

New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or
PT for genetic analysis of individuals with genetic disorders
PS Claim 11; Figure 114; 218pp; English.

CC This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The
CC invention also comprises a method for producing the proteins of the
CC invention by recombinant means and antibodies specific for the protein
CC of the invention. The antibody may be used for detecting the PRO
CC proteins of the invention and may be used to modify their activity.
CC polynucleotides may be used as hybridisation probes for a cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to
CC construct hybridisation probes for mapping the gene which encodes that
CC PRO and for genetic analysis of individuals with genetic disorders, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knock-out animals which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides are useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. The sequences may
CC also be used to detect overexpression on PRO polypeptides in cancerous
CC tumours and for screening for differentially expressed genes using
CC microarray technology. The present sequence represents a human PRO
CC protein of the invention.

Sequence 231 AA:

Query Match 85.0%; Score 1213; DB 23; Length 231;

Best Local Similarity 87.8%; Pred. No. 5.2e-113;

Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPKCFGLFLISFPLTGVAGTQSTHESLKPQRYVQFOSRNFNHILOMOPGRALTGSSVYF 60
DB 2 MPKCFGLFLISFPLTGVAGTQSTHESLKPQRYVQFOSRNFNHILOMOPGRALTGSSVYF 61
QY 61 VOYKIMFSCMKSSHQKPSGCMQHOISCFNPGCRITLAKYQGRQWKNKEDCWGTQELSCDIT 120
DB 62 VOYKI-----YGRQWKNKEDCWGTQELSCDIT 89
QY 121 SETSDIOEPYGRVRAASAGSYSEMSMTPTPTPWETKIDPPVNNITQVNSLVLITLAP 180
DB 90 SETSDIOEPYGRVRAASAGSYSEMSMTPTPTPWETKIDPPVNNITQVNSLVLITLAP 149
QY 181 NLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGARRAVEIEALTPHSSVCVYA 240

Db 150 NLPYRQKKNVSIEDYELLRYFVIINNSLEKEQKVEGAHRAVEIETALPHSSYCYVA 209
 QY 241 EIIYQPMIDRRSQRSEERCVEIP 262
 Db 210 EIIYQPMIDRRSQRSEERCVEIP 231

RESULT 11
 ID AAE17320 standard; Protein: 231 AA.
 XX AAE17320;
 AC AAE17320;
 XX
 DT 18-APR-2002 (first entry)
 XX
 DE Human cytokine receptor protein, sbg456548cytoRa #2.
 XX
 KW Human; therapy: wound healing disorder; vaccine; cancer; infection;
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
 KW depression; cardiovascular disease; myocardial infarction; renal failure;
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
 KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
 KW neuroptic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
 KW haemostatic; vulnerrary; anticonvulsant; antineumatic; neuroprotective;
 KW nephrotropic; hypotensive; vasotropic; cytosolic; cerebroprotective;
 KW allergy; cytokine receptor.
 XX
 OS Homo sapiens.
 PN WC200198342-A1.
 XX
 PD 27-DEC-2001.
 XX
 PF 22-JUN-2001; 2001WO-US19929.
 XX
 PR 22-JUN-2000; 2000US-213156P.
 XX
 PR 22-JUN-2000; 2000US-213161P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 AA Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
 Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
 WPI: 2002-139783/18.
 DR N-PSDB: AAD27815.
 XX
 PT Novel secreted and membrane-associated polypeptides and polynucleotides
 PT useful for preventing, ameliorating or correcting dysfunction or
 PT disease including diabetes, cancer, hypertension and growth
 PT abnormalities -
 XX
 PS Claim 1; Page 132-133; 138pp; English.

CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
 CC graft verse host disease, ischaemia, stroke, acute respiratory disease
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
 CC brain disorders including paraspinal nuclear palsy, myotonic dystrophy,
 CC depression, anxiety disorders and sleep disorders, cardiovascular
 CC diseases including congestive heart failure and myocardial infarction,
 CC respiratory diseases including chronic obstructive pulmonary disease,
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders
 CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
 CC and tendinitis, gastrointestinal diseases including intestinal
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
 CC reproductive diseases including low testosterone and male infertility.
 CC The present sequence is human cytokine receptor.
 XX
 SQ Sequence 231 AA:
 XX
 Query Match 85.0%; Score 1213; DB 23; Length 231;
 Best Local Similarity 87.8%; Pred. No. 5, 2e-113;
 Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
 QY 1 MPKHCFGLFLLIFELNGVAGTOSTHESLKPQVQFOSRNFHILQWPGRALTGNSSYVF 60
 Db 2 MPRHCFGLFLLIFELNGVAGTOSTHESLKPQVQFOSRNFHILQWPGRALTGNSSYVF 61
 QY 61 VQYKMFSCMSKSHQKPSGCMQHISCFQCRFLAKYGRQKRNKEDCKTQELSCDLT 120
 Db 62 VQYKI-----YGRQWKNKEDCKWQELSCDLT 89
 QY 121 SETSDIOEPYGRVRAASAGSYSEMSPTPTPMWETKIDPPVANNITQVNSLLVITLHAP 180
 Db 90 SETSDIOEPYGRVRAASAGSYSEMSPTPTPMWETKIDPPVANNITQVNSLLVITLHAP 149
 QY 181 NLPYRQKKNVSIEDYELLRYFVIINNSLEKEQKVEGAHRAVEIETALPHSSYCYVA 240
 Db 150 NLPYRQKKNVSIEDYELLRYFVIINNSLEKEQKVEGAHRAVEIETALPHSSYCYVA 209
 QY 241 EIIYQPMIDRRSQRSEERCVEIP 262
 Db 210 EIIYQPMIDRRSQRSEERCVEIP 231

RESULT 12
 ID AAE17319 standard; Protein: 214 AA.
 XX AAE17319;
 AC AAE17319;
 XX
 DT 18-APR-2002 (first entry)
 XX
 DE Human cytokine receptor protein, sbg456548cytoRa #1.
 XX
 KW Human; therapy: wound healing disorder; vaccine; cancer; infection;
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
 KW depression; cardiovascular disease; myocardial infarction; renal failure;
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
 KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
 KW neuroptic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
 KW haemostatic; vulnerrary; anticonvulsant; antineumatic; neuroprotective;
 KW nephrotropic; hypotensive; vasotropic; cytosolic; cerebroprotective;
 KW allergy; cytokine receptor.
 XX
 OS Homo sapiens.
 PN WC200198342-A1.
 XX

Db	1	TQSHESLAKPRVQFQSNFINILQNGRALRGNSSVYVQYKI	-----	45
Oy	81	CWQHSICNFPEGCRFLAKYQGRQMRKNKEDCWMGLOELSCDLTSETSIDIEPYGRYRASAG	140	
Db	46	-----YQGRQMRKNKEDCWMGLOELSCDLTSETSIDIEPYGRYRASAG	88	
Oy	141	SYSTEMSMPRTTPMWERKIDIPPPVNNITQVNSLVLITLHAPLPLRYQKERNVSIEDYEL	200	
Db	89	SYSTEMSMPRTTPMWERKIDIPPPVNNITQVNSLVLITLHAPLPLRYQKERNVSIEDYEL	148	
Oy	201	LYRVFTINNSLEKEQKYEGAGRAVEIEALPHSSYCVVAETIYQPMIDRRSORSEERCVE	260	
Db	149	LYRVFTINNSLEKEQKYEGAGRAVEIEALPHSSYCVVAETIYQPMIDRRSORSEERCVE	208	
Oy	261	IP 262		
Db	209	IP 210		
UT	14			
Db	2458			
XX	AAE02458	standard; Protein; 249 AA.		
XX	AAE02458;			
XX	10-AUG-2001	(first entry)		
DT				
XX		Human DNAX cytokine receptor subunit 4.1 (DCRS4.1).		
De				
XX				
KW		Human; immunomodulator; DNAX cytokine receptor subunit 4.1; DCRS4.1;		
KW		therapy; immunological disorder; drug screening; cell development;		
KX		chromosome 6q24.1-25.2.		
XX				
OS		Homo sapiens.		
XX				
FH	Key	Location/Qualifiers		
FT	Peptide	1..21		
FT	Protein	/label= Signal-peptide		
FT		22..249		
FT		/label= DCRS4.1		
FT		/note= "Human mature DNAX cytokine receptor subunit 4.1"		
FT	Modified-site	24		
FT		/note= "CR2 phosphorylation site"		
FT	Modified-site	25		
FT		/note= "Calcium phosphorylation site"		
FT	Modified-site	28		
FT		/note= "PKC phosphorylation site"		
FT	Domain	31..70		
FT		/label= cytokine_receptor_domain		
FT	Modified-site	51		
FT		/note= "cAMP PK site"		
FT	Modified-site	56		
FT		/note= "N-glycosylated"		
FT	Disulfide-bond	78..86		
FT		/label= Conserved_disulfide_linkage		
FT	Modified-site	81		
FT		/note= "Calcium phosphorylation site"		
FT	Modified-site	85		
FT		/note= "Calcium phosphorylation site"		
FT	Modified-site	89		
FT		/note= "Calcium phosphorylation site"		
FT	Modified-site	92		
FT		/note= "Calcium phosphorylation site"		
FT	Modified-site	100		
FT		/note= "Amdation site"		
FT	Modified-site	110		
FT		/note= "Myristoyl site"		
FT	Modified-site	118		
FT		/note= "PKC phosphorylation site"		
FT	Modified-site	119		
FT		/note= "cAMP phosphorylation site"		
FT	Modified-site	119		

FT	Modified-site	124	/note= "cAMP PK site"
FT	Modified-site	127	/note= "Myristoyl site"
FT	Modified-site	127	/note= "cAMP PK site"
FT	Modified-site	152	/note= "N-glycosylated"
FT	Modified-site	157	/note= "N-glycosylated"
FT	Modified-site	177	/note= "cAMP PK site"
FT	Modified-site	178	/note= "N-glycosylated"
FT	Modified-site	180	/note= "Calcium phosphorylation site"
FT	Modified-site	180	/note= "CK2 phosphorylation site"
FT	Modified-site	195	/note= "N-glycosylated"
FT	Modified-site	197	/note= "Calcium phosphorylation site"
FT	Modified-site	207	/note= "Myristoyl site"
FT	Modified-site	238	/note= "PKC phosphorylation site"
FT	Modified-site	241	/note= "Calcium phosphorylation site"
XX	W0200136467-A2.		
XX	25-MAY-2001.		
XX	16-NOV-2000; 2000WO-US31363.		
XX	18-NOV-1999; 99US-0443060.		
XX	13-DEC-1999; 99US-0170320.		
XX	(SCHE) SCHERING CORP.		
XX	Gorman DM;		
XX	WPI: 2001-343800/36.		
XX	N-PSDB: AAD06410.		
XX	New mammalian receptor proteins related to cytokine receptors, useful for regulating cell development and for diagnosis and treatment of immunological disorders		
XX	Claim 3; Page 22; 124pp; English.		
XX	The present sequence is human DNAX cytokine receptor subunit 4.1 (DCRS4.1). DCRS4 gene is located on chromosome 6q24.1-25.2. Cytokine receptors, fragments and antibodies are useful for treating immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are useful in drug screening to identify compounds having binding affinity to the receptor subunit. Modulators of DCRS are useful for modulating the physiology and development of a cell or tissue culture cells. A purified DCRS is useful as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to production of antibody to the endogenous receptor. Cytokine receptor sequences are useful as probes for detecting levels of the cytokine receptor in patients suspected of having an immunological disorder. Antibodies have therapeutic value, are useful as potent antagonist, in detecting or quantifying ligands, for isolating DCRS proteins and peptides, to screen expression libraries for particular expression products, to raise anti-idiotypic antibodies and for detecting or diagnosing various immunological conditions related to expression of the protein or cells which express the protein.		
XX	Sequence 249 AA;		
Query Match	73.2%;	Score 1045;	DB 22; Length 249;
Best Local Similarity	74.4%;	Pred. No. 3.8e-96;	

Matches 209; Conservative 3; Mismatches 17; Indels 52; Gaps 4;

QY 1 MKHCFELFLISFFLTGAGTOSTHESLKPQVOPQSRNFHILQMOGRALTGSSVYF 60
 DB 2 MKHCFELFLISFFLTGAGTOSTHESLKPQVOPQSRNFHILQMOGRALTGSSVYF 61
 QY 61 VOYKMFCSMKSSHQKSGCQWQHSICNPGCRLAKYGOQKQKNEKQWQELSCDLT 120
 DB 62 VOYKMFCSMKSSHQKSGCQWQHSICNPGCRLAKYGOQKQKNEKQWQELSCDLT 89
 QY 121 SETSDIOEPYGRVRAASAGSYSEMS-----MPTPTPWE--TKIDP 161
 DB 90 SETSDIOEPYGRVRAASAGSYSEMS-----MPTPTPWE--TKIDP 148
 QY 162 PVMNITQVNGSLVILHAPNLPYRYQKKNVSIEDYELLYRVFLINNSLEKQKVEGA 221
 DB 149 PVMNITQVNGSLVILHAPNLPYRYQKKNVSIEDYELLYRVFLINNSLEKQKVEGA 208
 QY 222 HRAVEIEALTPHSSYCYVAETIYQPMIDRRSQRSEECVEIP 262
 DB 209 HRAVEIEALTPHSSYCYVAETIYQPMIDRRSQRSEECVEIP 249

RESULT 15
 AA017380 standard; Protein; 249 AA.
 AA017380;

08-AUG-2002 (first entry)

Human cytokine receptor variant 1.

Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
 rheumatoid arthritis; multiple sclerosis; Crohn's disease;
 ulcerative colitis; transplant rejection; abortion; antipsoriatic;
 immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
 antiinflammatory; antitumor; cytosolic; dermatological;
 chromosome 6q24.1-25.2; receptor.

Homo sapiens.

EP191035-A2.

27-MAR-2002.

24-AUG-2001; 2001EP-0250307.

25-SEP-2000; 2000DE-1048626.

17-NOV-2000; 2000DE-1058907.

19-DEC-2000; 2000DE-1064906.

(SCHD) SCHERING AG.

Weiss B, Sabat R, Assadullah K, Toshi L;

WPI; 2002-332210/37.

N-PSDB; AAL45999.

New nucleic acid encoding soluble cytokine receptor, useful for

diagnosis and treatment of e.g. immune disease, also related protein

and antibodies

Claim 6; Page 12-13; 21pp; German.

The present invention provides the protein and coding sequences of 3
 variants of a human cytokine receptor. The sequences can be used in the
 diagnosis, prevention and treatment of immune diseases, including
 psoriasis, cancer, chronic/life-threatening infections, rheumatoid
 arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
 transplant rejection and in reproductive medicine, e.g. for diagnosing
 abnormal immune reactions which cause abortions. The present sequence is
 variant 1 of the invention.

XX SQ Sequence 249 AA;
 Query Match 73.2%; Score 1045; DB 23; Length 249;
 Best Local Similarity 74.4%; Pred. No. 3,8e-96;
 Matches 209; Conservative 3; Mismatches 17; Indels 52; Gaps 4;

QY 1 MKHCFELFLISFFLTGAGTOSTHESLKPQVOPQSRNFHILQMOGRALTGSSVYF 60
 DB 2 MKHCFELFLISFFLTGAGTOSTHESLKPQVOPQSRNFHILQMOGRALTGSSVYF 61
 QY 61 VOYKMFCSMKSSHQKSGCQWQHSICNPGCRLAKYGOQKQKNEKQWQELSCDLT 120
 DB 62 VOYKMFCSMKSSHQKSGCQWQHSICNPGCRLAKYGOQKQKNEKQWQELSCDLT 89
 QY 121 SETSDIOEPYGRVRAASAGSYSEMS-----MPTPTPWE--TKIDP 161
 DB 90 SETSDIOEPYGRVRAASAGSYSEMS-----MPTPTPWE--TKIDP 148
 QY 162 PVMNITQVNGSLVILHAPNLPYRYQKKNVSIEDYELLYRVFLINNSLEKQKVEGA 221
 DB 149 PVMNITQVNGSLVILHAPNLPYRYQKKNVSIEDYELLYRVFLINNSLEKQKVEGA 208
 QY 222 HRAVEIEALTPHSSYCYVAETIYQPMIDRRSQRSEECVEIP 262
 DB 209 HRAVEIEALTPHSSYCYVAETIYQPMIDRRSQRSEECVEIP 249

Search completed: December 22, 2002, 10:10:49
 Job time : 68 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 22, 2002, 10:08:17 ; Search time 44 seconds

(without alignments)
572.437 Million cell updates/sec

Title: US-09-964-994-2

Perfect score: 1427

Sequence: 1 MPNHCEFLGFLISFFLTGVAG.....YQPMIDRRSRQSERECVEIP 262

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR-73:*
2: PIR:*
3: PIR:*
4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164.5	11.5	575	2 A49667	Interleukin-10 rec
2	163	11.4	295	1 KFH03	tissue factor prec
3	158	11.1	560	2 J27387	interferon alpha r
4	156	10.9	349	2 JC6311	interferon recepto
5	152.5	10.7	578	2 I56215	Interleukin-10 rec
6	149.5	10.5	325	2 A47003	cytokine receptor
7	138.5	9.7	292	1 KFB03	tissue factor prec
8	136.5	9.6	557	2 A32694	interferon alpha/b
9	134.5	9.4	590	2 A45283	interferon alpha/b
10	132.5	9.3	292	1 KFRB3	tissue factor prec
11	122.5	8.6	489	2 A31555	interferon gamma r
12	122	8.5	294	1 KFM53	interferon gamma r
13	110.5	7.3	332	2 A49847	interferon gamma r
14	103.5	7.3	515	2 I39073	interferon alpha/b
15	101.5	7.1	331	2 A54295	interferon alpha/b
16	101.5	7.1	331	2 S59501	interferon recepto
17	92	6.4	337	2 I38500	interferon gamma r
18	90	6.3	1253	1 VHW	structural polypro
19	88	6.2	755	2 S42622	structural polypro
20	87.5	6.1	674	2 B4722	Kallmann syndrome
21	87.5	6.1	676	2 B47222	Kallmann syndrome
22	87	6.1	1145	2 S37136	hypothetical prote
23	86	6.0	477	2 T02748	interferon gamma r
24	86	6.0	477	2 A34368	ribonucleoside-dip
25	85	6.0	792	2 S16680	probable phospholip
26	85	6.0	810	2 E71550	RNA binding protei
27	84.5	5.9	703	2 T41065	probable transcript
28	84.5	5.9	1059	2 T13928	probable transcript
29	84.5	5.9	1083	2 T13929	probable transcript

30	83	5.8	266	2 I36855	gene B9R protein -
31	83	5.8	479	2 T02623	hypothetical prote
32	82.5	5.8	478	1 LEBED	hemolysin export s
33	82.5	5.8	650	2 T15972	hypothetical prote
34	81.5	5.7	456	2 B86834	sensor protein kin
35	81	5.7	430	2 T25489	hypothetical prote
36	81	5.7	564	2 T21423	hypothetical prote
37	81	5.7	810	1 S57196	calpain (EC 3.4.22
38	81	5.7	810	1 VHWV2	structural polypro
39	80.5	5.6	478	2 S10058	hemolysin secretio
40	80.5	5.6	527	2 T02128	beta-glucosidase h
41	80	5.6	426	2 JC7773	IL-13alpha 1 prot
42	80	5.6	582	2 A32034	choline kinase (EC
43	80	5.6	884	2 T01041	hypothetical prote
44	79.5	5.6	1286	2 AF0911	probable exported
45	79	5.5	335	2 AG2311	hypothetical prote

ALIGNMENTS

RESULT 1

A49667 Interleukin-10 receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000

C:Accession: A49667

R:Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W.

Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993

A:Title: A receptor for interleukin 10 is related to interferon receptors.

A:Reference number: A49667; MUID:94068585; PMID:8248239

A:Accession: A49667

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-575 <RES>

A:Cross-references: GB:L12120; MUID:9437615; PIDN:AA16156.1; PID:9437616

C:Genetics:

A:Gene: IL10r

C:Superfamily: Interleukin-10 receptor IL10R

C:Keywords: cytokine receptor

Query Match 11.5%; Score 164.5; DB 2; Length 575;

Best Local Similarity 26.7%; Pred. No. 1.4e-06;

Matches 74; Conservative 37; Mismatches 89; Indels 77; Gaps 16;

QY	6	FLGFLISFLTGYA-GTOSTHESLKPQVQFSRNFNITIQWOPGRALTGNSVYEVQYK 64
DB	8	FLVTISLSLEFLAYGT---ELDPSYVWFARFQHIHMKP--IPNOSSESY---YE 58
QY	65	IMFSCSMKSSHOKPSCGWOHISCNFGCRTLAKYGGQWKNKEDCWGTQELSCDTSETS 124
DB	59	V-----ALKQYGNSTWMDHICRAQALSCDTFTTL 90
QY	125	DIQEPYGG---RYRAASAGSYSEWSMT-PRFTPMWETKIDPPVNNITOV-----NGSLV 175
DB	91	DIYHRSYGYRARRAVDNSQSNMTTETFRFT-----VDEVILITVDSVTLKAMDGIYIG 144
QY	176	ILHAPLPYRQYKKNVSTEDYELLY---RVFTINNSLEKEQYVGARAVEIEALT- 231
DB	145	TIHP-----RPTTPAGDEYEQFKDLRYVKI--SIKRFSEL-KNAKRVKQETFTL 194
QY	232	---PHSSYCVVAETIYQPMIDRR---SORSEECVEI 261
DB	195	TVPIGVKRCVAV---LPRLSEIRINKAENSEECCLII 228

RESULT 2

KFH03 tissue factor precursor [validated] - human

N:Alternate names: coagulation factor III

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Dec-2000

C:Accession: A43645; A47574; A28320; A29062; A29672; A29008

R:MacKaman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
 Biochemistry 28, 1755-1762, 1989
 A>Title: Complete sequence of the human tissue factor gene, a highly regulated cellular
 A:Reference number: A43645; MUID:89247359; PMID:2719931
 A:Accession: A43645
 A:Molecule type: DNA
 A:Residues: 1-295 <MAC>
 A:Cross-references: GB:J02846; NID:9339505; PIDN:AAA61152.1; PID:9339506
 R:Fishner, K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn, R.M.
 Thromb. Res. 48, 89-99, 1987
 A>Title: Cloning and expression of human tissue factor cDNA.
 A:Reference number: A47574; MUID:881004453; PMID:3424286
 A:Accession: A47574
 A:Molecule type: mRNA
 A:Residues: 1-295 <FIS>
 A:Cross-references: GB:M27436; NID:9339507; PIDN:AAA61734.1; PID:9339508
 R:Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K.R.; Guha, A.; Kraus, J.; Li
 Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987
 A>Title: Isolation of cDNA clones coding for human tissue factor: primary structure of t
 A:Reference number: A94171; MUID:87260946; PMID:3037536
 A:Accession: A28320
 A:Molecule type: mRNA
 A:Residues: 1-295 <SP1>
 A:Cross-references: GB:J02931; NID:9339501; PIDN:AAA61150.1; PID:9339502
 R:Morrissey, J.H.; Fakhrai, H.; Edgington, T.S.
 Cell 50, 129-135, 1987
 A>Title: Molecular cloning of the cDNA for tissue factor, the cellular receptor for the
 A:Reference number: A29062; MUID:87244317; PMID:33297348
 A:Accession: A29062
 A:Molecule type: mRNA
 A:Residues: 1-295 <MOR>
 A:Cross-references: GB:J02931; NID:9339501; PIDN:AAA61150.1; PID:9339502
 A:Note: part of this sequence, including the amino end of the mature protein, was confin
 R:Scarpelli, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.; Flendermeyer, R.R.; Siegel,
 Biochemistry 26, 5234-5238, 1987
 A>Title: Human tissue factor: cDNA sequence and chromosome localization of the gene.
 A:Reference number: A29672; MUID:88050796; PMID:2823875
 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
 Biochemistry 27, 4227-4231, 1988
 A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyte
 A:Reference number: A37422; MUID:8900604; PMID:3165978
 A:Contents: annotation; disulfide bonds and fatty acid binding site
 C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
 Biochemistry 27, 4227-4231, 1988
 A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyte
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 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
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 A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyte
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 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
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 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
 Biochemistry 27, 4227-4231, 1988
 A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyte
 A:Reference number: A37422; MUID:8900604; PMID:3165978
 A:Contents: annotation; disulfide bonds and fatty acid binding site
 C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
 Biochemistry 27, 4227-4231, 1988
 A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyte
 A:Reference number: A37422; MUID:8900604; PMID:3165978
 A:Contents: annotation; disulfide bonds and fatty acid binding site
 C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
 Biochemistry 27, 4227-4231, 1988
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 A:Contents: annotation; disulfide bonds and fatty acid binding site
 C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
 Biochemistry 27, 4227-4231, 1988
 A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyte
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 A:Contents: annotation; disulfide bonds and fatty acid binding site
 C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
 Biochemistry 27, 4227-4231, 1988
 A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyte
 A:Reference number: A37422; MUID:8900604; PMID:3165978
 A:Contents: annotation; disulfide bonds and fatty acid binding site
 C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
 Biochemistry 27, 4227-4231, 1988
 A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyte
 A:Reference number: A37422; MUID:8900604; PMID:3165978
 A:Contents: annotation; disulfide bonds and fatty acid binding site
 C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
 A:Accession: A29672
 A:Molecule type: mRNA
 A:Residues: 1-259, 'A', 261-295 <SCA>
 A:Cross-references: GB:M16553; NID:9339503; PIDN:AAA61151.1; PID:9339504
 R:Bach, R.; Konigsberg, M.H.; Nemerson, Y.
 Biochemistry 27, 4227-4231, 1988
 A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyte
 A:Reference number: A37422; MUID:8900604; PMID:3165978
 A:Contents: annotation; disulfide bonds and fatty

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70 SMKSHQKPSCKMWHISCNFGCGCTLAKYGGORKNRKNEDGTOELSCDILNISE--TSIDQE 128
   ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db STKSG-----DMKSK--CEYTDTBEDLDIDEIKVDKQ 101

129 PYGRV-----RAASAGSYSE--WSMTPRETPWMEKTI-DPVVNITQVNGSLYLIIHA 179
   ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db TYLARVFSPAGNVESTGSAGEPTLENSPEFTPYDETNIIGOPTIOSFEOGVTKVNTVED 161

180 PNLPRYRKKEKNVSIEDYY--ELLYRVLIINSLSLEDEQKYEGGAHR-AVEITALPHSSY 236
   ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db ERLTVR-RNNTFILSRDFGFKDLTYTLIYMKWSSSGKTAKTINFEPLIDV---KGENV 217

OY 237 C-VVAETIYOPMLDRRSQRSEERCY 259
Db 218 CFSTQAIVIPSTRVTNRKSDPSPECM 242

RESULT 3
Interferon alpha receptor type 1 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
A:Accession: S27387; S33770
P:Mouchel-Viehn, E.; Luftalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A>Title: Specific antiviral activities of the human alpha interferons are d
A:Reference number: S27387; MUID:93076908; PMID:1446745
A:Accession: S27387
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-560 <MOD>
A:Cross-references: EMBL:X68443; NID:g431; PIDN:CAA8484.1; PID:g432
A:Experimental source: MDBK cells
R:Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A>Title: Cloning and characterization of a bovine alpha interferon receptor
A:Reference number: S33770; MUID:93305725; PMID:8318540
A:Accession: S33770
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-421,'V',423-560 <DIM>
A:Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA2571.1; PID:g163188
A:Experimental source: lung
A:Keywords: antiviral; cytokine receptor; transmembrane protein
E:1-24/Domains: signal sequence #status predicted <SIG>
F:25-560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

Query Match 11.1%; Score 158; DB 2; Length 560;
Best Local Similarity 24.1%; Pred. No. 5e+06;
Matches 57; Conservative 38; Mismatches 100; Indels 42; Gaps

OY 21 TOSTHSLRPKRQPOFSRNFHNLLMQPGALGNSSVVYQVKIMFSCMSKSHQPSG 80
   ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db 223 TTRHVPSPENIQIADNOIYLKMD---VREYNATPAOWLRAFKKIPGNHSD--- 275

OY 81 CMOHICSNFPGCRTLAKYGORKNRKNEDCGTDELSCDILTSETSIDOEPPYGYRAASAG 140
   ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db 276 -----KKKIPIPCNCNWTSTHCVPFREVS--RGIIYVRYRASGN 313

OY 141 SYSSESMTPRETPTWMEKTDIDPVANITQV--NGSILVLIHPNLPRYRKQEKNNVSIEDYE 199
   ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db 314 GTFWSEEKEEFNTEMKTTIFPPVIYSKVSTDSDLSHVSGAS-----EESENMSVNOLYP 367

OY 200 LYKRVLTINSLSLEKDEKYGVGARAVETIALFLPHSSVCVAETIYQPMI---DRSQRS 254
   ||| | : : : : ||| | : : : : ||| | : : : : ||| | : : : :
Db 368 LIYEIVFWENTISAEKRVLEKRTNFI-FPDLPKLTYCYCAK---RALIEDRRNRKKS 420

RESULT 4
JG6311
Interferon receptor class II cytoic receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
```

C:Accession: JC6311
 R:Gibbs, V.C.; Pennica, D.
 Gene 186, 97-101, 1997
 A:Title: CRE2-4: isolation of cDNA clones encoding the human and mouse proteins.
 A:Reference number: JC6311; MUID:97199375; PMID:9047351
 A:Accession: JC6311
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-349 <GIB>
 A:Cross-references: GB:U53696

Query Match 10.9%; Score 156; DB 2; Length 349;
 Best Local Similarity 26.8%; Pred. No. 4.1e-06;
 Matches 72; Conservative 30; Mismatches 89; Indels 78; Gaps 13;

QY 5 CELGLIFLFFLTGAGTOSTHESLKPRQVQOSRNFHNLQWQ-----PERALTGSSVYF 60
 DB 4 CVAGWLGFLVLPALGMP-----PPEKVRMNSVFNKNIQWVEVAFKPTNLT-----FT 53
 61 VQYKIMFS-----CSMKSSHQPCGCMQHISCNFCRTLAKGQRMKNKEDCWGTQELS 116
 54 AQVEYRFRFOHCKRTASTQ-----CDF-----SHLSKTD----- 84
 QY 117 CDLTSESDIDEPYGRVRAASAGSYSEMSMTPRFTPWETKIDPPVNNITOVNGLLVI 176
 DB 85 -----YTVRVAELADESEM-VNVTFCPEVDITIGPEMQIESLASLELR 130
 QY 177 LHAPMLPRYQKE-----KNVSIEDYELLYRV-FIINNSLEKQKYEGCAHRAVEIEA 229
 DB 131 FSAPI-----NNEPTWTLKNI-----YDSMAYRQYKMGNTNEKQVY--SPYSEVLRN 180
 QY 230 LTPHSSCYVAEIIYQPMIDRRSQRSEERC 258
 DB 181 LEPWTTCIQVQGFLLDQNRGEMSEPIC 209

RESULT 5

Interleukin-10 receptor - human
 C:Accession: 156215
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000
 C:Species: Homo sapiens (man)
 C:Accession: 156215
 J: Liu, Y.; Wei, S.H.; Ho, A.S.; de Maal Malfeyt, R.; Moore, K.W.
 J: Immunol. 152, 1821-1829, 1994
 A:Title: Expression cloning and characterization of a human IL-10 receptor.
 A:Reference number: 156215; MUID:94165477; PMID:8120391
 A:Accession: 156215
 Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-578 <RES>
 A:Cross-references: EMBL:U00672; NID:9482802; PIDN:AA17896.1; PID:9482803
 C:Genetics:
 A:Gene: GDB: IL10R; HL-10R
 A:Cross-references: GDB:330958; OMIM:146933
 A:Map position: 11q23.3-11q23.3
 A:Superfamily: Interleukin-10 receptor IL10R
 C:Keywords: cytokine receptor

Query Match 10.7%; Score 152.5; DB 2; Length 578;
 Best Local Similarity 24.5%; Pred. No. 1.6e-05;
 Matches 67; Conservative 39; Mismatches 94; Indels 73; Gaps 14;

QY 7 LGFLISFFLTGVA-GTOSTHESLKPRQVQOSRNFHNLQWQGRALTGSSVYFQYKI 65
 DB 9 LAALISLRIGSDAGT-----ELSPPSVWFPAEFFHHLHTP----- 47
 QY 66 MFCSSMSSHQKPSGQOHISCNFGCRTLAKYGRQRMKNKEDCWGTQELSCLDITSETSD 125
 DB 48 -----IPNQSESTCYE-----VALRGIENSNISNC--SOTLSYDLTAVYLD 89
 QY 126 I--QEPYGRVRAASAGSYSEMSMT-PRFTPWETKIDPPVNNITOV-----NSGLVIL 177
 DB 90 LYHNGYRVRRAVADGSRHSMVYTNTRFS-----VDEVTLTGVSVALTEIHNGFIIIGKI 143

QY 178 HAPMLPRYQKEKNYSIEDYELLYRV-FIINNSLEKQKYEGCAHRAVEIEALTPHSS- 235
 DB 144 QLP-----RPMAPANTYESIFSHFREYELAIKRGVGNFTFKKVKHNFSLITSG 196
 QY 236 ----CYVAEIIYQPMIDRRSOR---SEERCVEI 261
 DB 197 EVGEFCVQY---KPSVASNSKMGMSKECISL 226

RESULT 6

A47003
 Cytokine receptor family class II protein CRE2-4 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 01-Dec-2000
 C:Accession: A47003; G01418
 R: Imitfalia, G.; Gardiner, K.; Uze, G.
 Genomics 16, 366-373, 1993
 A:Title: A new member of the cytokine receptor gene family maps on chromosome 21 at 1
 A:Reference number: A47003; MUID:93300510; PMID:8314576
 A:Accession: A47003
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-325 <LUT>
 A:Cross-references: GB:Z17227; NID:9393378; PIDN:CAA78933.1; PID:9393379
 R: Imitfalia, G.
 Submitted to the EMBL Data Library, April 1994
 A:Reference number: G06935
 A:Accession: G01418
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-123, 'D', 125-268, 'VGRME' <LUT>
 A:Cross-references: EMBL:U00898; NID:9571295; PID:9571296
 C:Genetics:
 A:Gene: GDB: CRE2-4
 A:Cross-references: GDB:138168; OMIM:123889
 A:Map position: 21q; 21q22.1-21q22.2
 A:Introns: 17/1; 58/2; 111/1; 166/3; 216/1
 C:Keywords: transmembrane protein

Query Match 10.5%; Score 149.5; DB 2; Length 325;
 Best Local Similarity 24.1%; Pred. No. 1.4e-05;
 Matches 57; Conservative 32; Mismatches 89; Indels 59; Gaps 8;

QY 30 PQVQOSRNFHNLQWQGRALTN--SSVYFQYKIMFSCSMKSSHQKPSGQOHISC 87
 DB 24 PENYAMNSVNFENKIQWSPAFKGNLTFTAQYLSYRIF----- 62
 QY 88 NPPGRTLAKYGRQRMKNKEDCWGTQELSCLDITSETSDIQEPIYG---RVRAASAGSYS 143
 DB 63 -----QDKCMNTTLTECDFSSLSK-----YGDHTLRVRAEFADHS 98
 QY 144 EMSMTPRFTPWETKIDPPVNNITOVNGLVILHAPMLPRYQ--KEKNYSIEDYELL 201
 DB 99 DW-VNITFCPPVDITIGPGQVLELADSLMKRFLAPINENYETWTKVY---YNSWT 153
 QY 202 YRVFIINNSLEKQKYEGCAHRAVEIEALTPHSSCYVAEIIYQPMIDRRSQRSEERC 258
 DB 154 YNVQWKNGTDEKFOITPQYDFEV-LRNLEPWTTCVQVGRGLPDRNKAAGMSSEFVC 209

RESULT 7

KFB03
 Tissue factor precursor - bovine
 N:Alternate names: coagulation factor III
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C:Accession: J01319
 R: Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
 Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
 A:Title: cDNA and amino acid sequences of bovine tissue factor.
 A:Reference number: J01319; MUID:92109720; PMID:11764065
 A:Accession: J01319

A:Accession: I48428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 426-445 <RE6>
A:Cross-references: EMBL:006242; NID:9497112; PIDN:AAA65007.1; PID:9755813
A:Accession: I48429
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 473-590 <RE7>
A:Cross-references: EMBL:006244; NID:9497114; PIDN:AAA65008.1; PID:9510265
C:Genetics:
A:Gene: IFNAR
A:Introns: 177/3; 331/1
C:Keywords: cytokine receptor; transmembrane protein

Query Match 9.4%; Score 134.5; DB 2; Length 590;
Best Local Similarity 21.4%; Pred. No. 0.00063;
Matches 45; Conservative 39; Mismatches 99; Indels 27; Gaps 7;

55 NSSVYFV--QKIMFGSCSMSSHQKPSGCMQHSNFCPCRTLAKY--GGROMKNKEDC 109
34 NIDVYITDNYTLK-----SSHGESMG-----SVTF-----AEYRTKDAKMLKVEPC 78
110 WGTQELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMTPEPTMWEKIDPPVANTQV 169
79 QHTTTKCEFSLLDTNVYIKQFRVRAEENSTSSWNEVDPIFYAHMSPEVRLAE 138
170 NSGLVILHAPNLPRYRKQEKVNSIEDYELLYRVFIINSLKEQKVEGAHRAVEIEA 229
139 DRAIVLHISPG-----DDGNMALEKPSFSYTIIRWQS--SSDKTKINSTIYVEKIE 191
230 LPHSSYCVVAEIQPMLDRSQSEERCY 259
192 LRPETTYCLEVKAIHPSLKNHSTVQCI 221

RESULT 10
KFR3
tissue factor precursor - rabbit
N:Alternate names: coagulation factor III
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C:Accession: J00441; S23681
R:Andrews, B.S.; Rehemtulla, A.; Fowler, B.J.; Edgington, T.S.; Mackman, N.
Gene 98, 265-269, 1991
A:Title: Conservation of tissue factor primary sequence among three mammalian species.
A:Reference number: J00441; MUID:91200676; PMID:1840552
A:Accession: J00441
A:Molecule type: mRNA
A:Residues: 1-292 <AND>
A:Cross-references: GB:M5390; NID:9165696; PIDN:AAA63469.1; PID:9165697
A:Experimental source: brain
R:Pasashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.; Konigsberg, W.
Thromb. Haemost. 66, 315-320, 1991
A:Title: Molecular cloning, characterization and expression of cDNA for rabbit brain tis
A:Reference number: S23681; MUID:92081032; PMID:1746002
A:Accession: S23681
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 33-292 <PAW>
A:Cross-references: EMBL:X53521; NID:91495; PIDN:CAA37597.1; PID:93980170
C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C:Superfamily: Expression of tissue factor can be induced in a variety of tissues by certain
C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F:1-32/Domain: signal sequence #status predicted <STG>
F:33-292/Product: tissue factor #status predicted <KAT>
F:250-271/Domain: extracellular #status predicted <EXT>
F:272-292/Domain: transmembrane #status predicted <XTM>
F:41,114,154,167,182/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:79-87,216-239/Disulfide bond: #status predicted
F:274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 9.3%; Score 132.5; DB 1; Length 292;
Best Local Similarity 22.2%; Pred. No. 0.00039;
Matches 62; Conservative 39; Mismatches 89; Indels 89; Gaps 13;

10 LISFFLTGVAGTGSTHESLKPQRVQFQSRNFHNLQOPGRALTGNSVYFVQKIMFSC 69
21 LIGWLIAQVARRADT--TGRAVNLVTKSTNFKTLEWEP-----KSIDHV-YTVQIST 70
70 SMKSSHQKPSGCMQHSNFCPCRTLAKYGOBOMKNKEDCWGTQELSCDLTSE--TSIOE 128
71 RLEN-----WKS--CFILAEITCDLTFDEVYKVDGQ 99
129 PYGGRY-----RAASAGSYSE--WSMTPEPTMWEKIDPPV-----MNTQVN 170
100 TYMARVLSPPARKNNTGPEEPFRNSPEPTFLDNLQOPTIQSPEQVGTKLNTVQD 159
171 GSLVILHAPNLPRY--YQEKVNSIEDYELLY-----RVFIINSLKEQKVEGA 221
160 ARVLVRRNGTFLSLRAVFGKDLN-----YTLVYKRASSGKATATTNTNEFLIDVKG 213
222 HRAVEIEALTPHSSYCVVAEIQPMLDRSQSEERCVE 260
214 NYCFSVOAVIPSR-----KKRQSPESILTE 238

RESULT 11
A31555
interferon gamma receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
C:Accession: A31555
R:Aguet, M.; Dembic, Z.; Meriin, G.
Cell 55, 273-280, 1988
A:Title: Molecular cloning and expression of the human interferon-gamma receptor.
A:Reference number: A31555; MUID:89003065; PMID:2971451
A:Accession: A31555
A:Molecule type: mRNA
A:Residues: 1-489 <AGU>
A:Cross-references: GB:J03143; NID:9184650; PIDN:AAA52731.1; PID:9306915
C:Genetics:
A:Gene: IFNGR1; IFNGR
A:Cross-references: GDB:120688; OMIM:107470
A:Map position: 6q23-6q24
C:Superfamily: Interferon gamma receptor
C:Keywords: cytokine receptor; transmembrane protein

Query Match 8.6%; Score 122.5; DB 2; Length 489;
Best Local Similarity 20.1%; Pred. No. 0.0057;
Matches 56; Conservative 49; Mismatches 103; Indels 71; Gaps 10;

9 FLISFFLTGVA-----GQSTHESL--KQVRQFQSRNFHNLQOPGRALTGNSVYFVQ 62
5 FLPLVMQGVRAEMGTADLPSSVPTPTNVTESYNNPIVYW-----E 49
63 YKIM-----FSCSMKSSHQKPSGCMQHSNFCPCRTLAKYGOBOMKNKEDCWGTQELSC 117
50 YQIMQVVFVEVKN-----YGVKSEWTDACINISHHC 85
118 DLTSSETSDIOEPYGRVRAASAGSYSEMSMTPEPTMWEKIDPPVANTQVNGSLVLT 177
86 NISHVQDPSNLSLWVRKARVQKESAVAKSEEFVACDGRKIGPKLDIRKEKQIMIDI 145
178 HAPNLPRYRKQEKVNSIEDY-----YELLRVFIINSLKEQKVE-----GAH 222
146 FHPSPV-FVNGDEQEV---DVPETTCYIRVNVYRANGSEIQYKILQKEDCDPEIQO 201
223 RAVEIEALTPHSSYCVVAEIQPMLDRSQSEERCVEI 261
202 LAIPVSSL--NSQYCSAEGVLHWGVTTTEKSEKVCITI 238

RESULT 12

KFM33
 tissue factor precursor - mouse
 N:Alternate names: coagulation factor III
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C:Accession: A32318; A39046
 R:Harrell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
 M:Cell Biol. 9, 2567-2573, 1989
 A:Title: A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a protein hc
 A:Reference number: A32318; MUID:89343974; PMID:2761539
 A:Accession: A32318
 A:Molecule type: mRNA
 A:Residues: 1-294 <HR>
 A:Cross-references: GB:M26071; NID:9201924; PIDN:AAA0414.1; PID:9201925
 R:Ranganathan, G.; Blatt, S.P.; Subramaniam, M.; Pass, D.N.; Mahle, N.J.; Getz, M.J.
 J. Biol. Chem. 266, 496-501, 1991
 A:Title: Cloning of murine tissue factor and regulation of gene expression by transformi
 A:Reference number: A39046; MUID:91093171; PMID:1985911
 A:Accession: A39046
 A:Molecule type: mRNA
 A:Residues: 1-25, 'I', 27-294 <RAN>
 A:Cross-references: GB:M57896; GB:J05713; NID:9201926; PIDN:AAA63400.1; PID:9201927
 A>Note: 26-Phr was also found
 C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
 C:Comment: Expression of tissue factor can be induced in a variety of tissues by certain
 C:Superfamily: tissue factor
 C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
 F:1-29/Domain: signal sequence #status predicted <SIO>
 F:30-294/Product: tissue factor #status predicted <MAT>
 F:30-251/Domain: extracellular #status predicted <EXT>
 F:252-274/Domain: transmembrane #status predicted <TMM>
 F:37,57,169,200/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:75-83,218-241/Disulfide bonds: #status predicted
 F:275/Binding site: palmitate (cys) (covalent) #status experimental
 Query Match 8.5%; Score 122; DB 1; Length 294;
 Best Local Similarity 22.7%; Pred. No. 0.0033;
 Matches 64; Conservative 36; Mismatches 100; Indels 82; Gaps 13;
 Oy 6 FLGLISFLVAGTOSTHESLKPORVOFOSRNFHNILOWGRALTGSSVYFVQYKI 65
 Db 17 FLGLL-LQVTAAGAIPE-----KAFNLWISTDFETILEMOP---KPTNYTYTVO--- 63
 Oy 66 MFSCSKSSHQKPSGOWHISCNFPCRTLAKYGOROMKKECCWGTQELSCDTLSE-TS 124
 Db 64 ---ISDRS-----RNMKKK--CFSTTDRECDLTDLIVK 91
 Oy 125 DIOEPYGRVRAASA-----GSYSEWSMTPTFTPMWETKIDPPV----- 163
 Db 92 DVTWVYEAKVLSPRRNSVHGDDQDLVIHGEPPFTVAPKFLRYRDTNLGQPVYQFEOD 151
 Oy 164 ---MNTQVNGSLIVLHAHPNLPYRQKENVSIEDYELLYRFTINNSLEKEQYEG 220
 Db 152 GRLNVVAKDSLTLVKKNGTFLRLROYFGKDLG---YITTYRK---GSSITGKKTINTNT 204
 Oy 221 ARAVEIEALTPHSYC--VVAETIQPMLDRRSORSEERCE 260
 Db 205 NEFSIDVE---EGVSYCFVQAMIFSRKTNQNSPGSSTVCTE 243
 RESULT 13
 AA9947
 interferon gamma receptor beta subunit - mouse
 N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type I
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A49947
 R:Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
 Cell 76, 803-810, 1994
 A:Title: A novel member of the interferon receptor family complements functionality of t
 A:Reference number: A49947; MUID:94170381; PMID:8124717
 A:Accession: A49947
 A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-332 <HEM>
 A:Cross-references: GB:S69336; NID:9545841; PIDN:AAB30165.1; PID:9545842
 A:Experimental source: early B-cell line Y16
 A>Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIPI:145656)
 C:Keywords: cytokine receptor
 Query Match 7.7%; Score 110.5; DB 2; Length 332;
 Best Local Similarity 20.2%; Pred. No. 0.04; 99; Indels 69; Gaps 11;
 Matches 51; Conservative 33; Mismatches 99;
 Oy 9 FLISFLVAGTOSTHESLK---PORVOFOSRNFHNILOWGRALTG--NSSVYFVQY 63
 Db 7 WLPSLLCGAAGAAASPDSPSQAAPLNPRHLVNDQDLTWEPSSSNDPRVYQVEY 66
 Oy 64 KMFSCSKSSHQKPSGOWHISCNFPCRTLAKYGOROMKKECCWGTQELSCDTL--S 121
 Db 67 SFI-----DSWRL-----EPNCDDITETKCDLTGGG 95
 Oy 122 ETSDIOEPY--YGRVRAASAGSYSEWSMTPTFTPMWETKIDPPV-MNTQVNGSLV--- 175
 Db 96 RLKLFPPHFTVFLVRAKRGMLTSKMGLEPFQHYENTVGPKNKISVTPGKGSIVHFS 155
 Oy 176 ---ILHAPNLPYRQKENVSIEDYELLYRFTINNSLEKEQYVEGAHR--AVEIEA 229
 Db 156 PPFDVFGATFQY-----LVHYME-----KSETQDQVGGPFRKSNISVLGN 196
 Oy 230 LTPHSSCYVAE 241
 Db 197 LKPYRYVCLQTE 208
 RESULT 14
 I39073
 interferon alpha-beta receptor, beta subunit long form - human
 C:Species: Homo sapiens (man)
 C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 01-Dec-2000
 C:Accession: I39073; S59502
 R:Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.; Pitka, P.; Colamo
 J. Biol. Chem. 270, 21606-21611, 1995
 A:Title: Cloning and expression of a long form of the beta subunit of the interferon
 A:Reference number: I39073; MUID:95394915; PMID:7665574
 A:Accession: I39073
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-515 <RES>
 A:Cross-references: EMBL:U29584; NID:993040; PIDN:AAC50202.1; PID:993041
 R:Infatalla, G.; Holland, S.J.; Ciano, E.; Monneron, D.; Reboul, J.; Rogers, N.C.; Sm
 EMBO J. 14, 5100-5108, 1995
 A:Title: Mutant USA cells are complemented by an interferon-alpha-beta receptor subun
 A:Reference number: S59501; MUID:96067138; PMID:7588638
 A:Accession: S59502
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-150, 'M', 152-515 <LUT>
 A:Cross-references: GB:L41942; NID:9995292; PIDN:AAB46413.1; PID:9995293
 C:Keywords: alternative splicing; cytokine receptor
 Query Match 7.3%; Score 103.5; DB 2; Length 515;
 Best Local Similarity 20.3%; Pred. No. 0.29;
 Matches 46; Conservative 39; Mismatches 99; Indels 43; Gaps 7;
 Oy 38 RNFHNILOWGRALTGSSVYFVQYKIMFSCSKSSHQKPSGOWHISCNFPCRTLAK 97
 Db 46 RNFRLISLSE-----LKNHSIVPTHYTLTYTMSK----- 75
 Oy 98 YGQRQKKNEDCWGTQELSCDTLSESDIOEPYGRVRAASAGSYSEWSMTPTFTPMWET 157
 Db 76 --PEDIKVVKNCANTRSCDLDLDEWRSHEAVY-IVLECFSSNTLFLFSGSHFWALIDM 132
 Oy 158 KIDPMNTQVNGSLIVLHAHPNLPYRQKENVSIEDYELLYRFTINNSLEKEQ 216
 Db 133 SFEPPFELVGTNNHNVVVKFPSIVEEELQFLSLVIEQSGIYK-----KHKPEIK 186

QY 217 VYEGAHRAVEIEALTPHSSVCVAEITYQPMIDRRSQ-RSEERCVEIP 262
Db 187 GMSGNFYIIDKLIPTNTVCV--SVYLEHSDQAVIKSPLKCTLLP 231

RESULT 15

A54295
Interferon alpha/beta receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999
C:Accession: A54295
R:Novick, D.; Cohen, B.; Rubinstein, M.
Cell 77, 391-400, 1994
A:Title: The human interferon alpha/beta receptor: characterization and molecular cloning
A:Reference number: A54295; MUID:94236684; PMID:8181059
A:Accession: A54295
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-331 <NOV>
A:Cross-references: GB:X77722; NID:9488363; PIDN:CA54785.1; PID:9488364
Keywords: cytokine receptor

Query Match 7.1%; Score 101.5; DB 2; Length 331;
Best Local Similarity 20.3%; Pred. No. 0.25;
Matches 46; Conservative 39; Mismatches 99; Indels 43; Gaps 7;
QY 38 RNHNILQWQPGALTGSSVYFVQKIMFSCSKSHOKPSGCMOHISCNFPDGCRTLAK 97
Db 46 RNRSLISWE----LKNHSIVPTHYTLTYTMSK----- 75
QY 98 YGQRQWKNKEDCGTQELSCDLTSETSDIOEPYGRVRAASAGSISEWNTPRFTPMWET 157
Db 76 --PEDLKVKNKANTRSFCDLTDEWRSTHEAVV-TVLEGFSGNTTLFSCSHNFWLAIDW 132
QY 158 KIDPPVYMITQVNGSLVILHAENL-PYRYQKEKNYSIDYELLRYVFIINNSLEKBOK 216
Db 133 SFEPPFEELVGFTHINWVVKFPSIVEEELQFDLSLVIEQSEGVAK-----KHKPEIK 186
QY 217 VYEGAHRAVEIEALTPHSSVCVAEITYQPMIDRRSQ-RSEERCVEIP 262
Db 187 GMSGNFYIIDKLIPTNTVCV--SVYLEHSDQAVIKSPLKCTLLP 231

Search completed: December 22, 2002, 10:14:23
Job time : 46 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 22, 2002, 09:12:37 ; Search time 25 Seconds
(without alignments)
434.672 Million cell updates/sec

Title: US-09-964-994-2

Perfect score: 1427
Sequence: 1 MPKHCFLGFLISFLTGAVG.....YQPMIDRRSQSEERCVEIP 262

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164.5	11.5	575	1 I10R_MOUSE	Q61727 mus musculus
2	163	11.4	295	1 TF_HUMAN	P13726 homo sapien
3	158	11.1	560	1 INR1_BOVIN	Q04790 bos taurus
4	156	10.9	349	1 I10S_MOUSE	Q61190 mus musculus
5	152.5	10.7	578	1 I10S_HUMAN	Q13651 homo sapien
6	149.5	10.5	325	1 I10S_HUMAN	Q08334 homo sapien
7	138.5	9.7	292	1 TF_BOVIN	P30931 bos taurus
8	136.5	9.6	289	1 TF_CAVPO	Q93108 cavia porce
9	136.5	9.6	557	1 INR1_HUMAN	P17181 homo sapien
10	136.5	9.6	560	1 INR1_SHEEP	Q28589 ovis aries
11	134.5	9.4	590	1 INR1_MOUSE	P33896 mus musculus
12	132.5	9.3	292	1 TF_RABIT	P24055 oryctolagus
13	128.5	9.0	295	1 TF_RAT	P42533 rattus norv
14	124	8.7	494	1 TF_MOUSE	P20352 mus musculus
15	122.5	8.6	128	1 INGR_HUMAN	P15260 homo sapien
16	115	8.1	536	1 INR2_SHEEP	Q95207 ovis aries
17	104	7.3	530	1 INR2_BOVIN	Q95141 bos taurus
18	101.5	7.1	515	1 INR2_HUMAN	P48551 homo sapien
19	92	6.4	337	1 INGS_HUMAN	P38464 homo sapien
20	92	6.4	1254	1 POLS_RRVT	P08491 roos river
21	90.5	6.3	424	1 KPSH_HUMAN	P11801 homo sapien
22	90	6.3	1253	1 POLS_SFV	P03315 semliki for
23	88.5	6.2	1170	1 TSP2_BOVIN	Q95116 bos taurus
24	87.5	6.1	676	1 KALM_CHICK	P33005 gallus galli
25	86	6.0	477	1 INGR_MOUSE	P15261 mus musculus
26	85	5.9	792	1 RIRI_HUMAN	P23921 homo sapien
27	84.5	5.9	274	1 VC06_SPYKA	P32226 swinepox vi
28	82.5	5.8	478	1 HLY4_ECOLI	P09966 escherichia
29	81	5.7	564	1 YUES_CAEEL	P90859 caenorhabdi
30	81	5.7	810	1 CAN3_CHICK	Q92177 gallus galli
31	81	5.7	1247	1 POLS_ONNVG	P22056 o'nyong-nyo
32	80.5	5.6	478	1 HLYD_ECOLI	P06739 escherichia
33	80	5.6	582	1 KICH_YEAST	P20465 saccharomyc

34	79.5	5.6	1411	1 Y297_HUMAN	O15040 homo sapien
35	79	5.5	410	1 CPX1_BACME	P14762 bacillus me
36	79	5.5	606	1 Z214_HUMAN	Q9159 homo sapien
37	78.5	5.5	576	1 GRK6_RAT	Q91711 rattus norv
38	78.5	5.5	760	1 YBIL_ECOLI	P75780 escherichia
39	78.5	5.5	1003	1 POL_HVINS	P12497 human immun
40	78	5.5	626	1 HCYD_EURCA	P02241 eurpelina c
41	78	5.5	1254	1 POLS_RRVN	P13890 roos river
42	77.5	5.4	526	1 CAT1_HUMAN	P04040 homo sapien
43	77.5	5.4	638	1 GHR_HUMAN	P10912 homo sapien
44	77.5	5.4	897	1 CYR2_HUMAN	P32927 homo sapien
45	77.5	5.4	1172	1 TSP2_HUMAN	P35442 homo sapien

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	AA
AC	061727	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Interleukin-10 receptor alpha chain precursor (IL-10R-A) (IL-10R1).				
GN	IL10RA OR IL10R.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
RN	NCBI_TaxID=10090;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6 X AJ F1; TISSUE=Hematopoietic;				
RA	MEDLINE=94068585; PubMed=8248239;				
FX	Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;				
RT	"A receptor for Interleukin 10 is related to interferon receptors."				
RL	Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).				
CC	- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.				
CC	- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.				
CC	-----				
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	-----				
DR	EMBL, L12120; AAA16156.1; -				
DR	MGD; MGI:96538; IL10ra.				
DR	Interpro; IPR000282; Cytok_receptor_2.				
KW	Receptor; Transmembrane; Glycoprotein; Signal.				
FT	SIGNAL	1	16	POTENTIAL.	
FT	CHAIN	17	575	INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.	
FT	DOMAIN	17	241	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	242	262	POTENTIAL.	
FT	DOMAIN	263	575	POTENTIAL.	
FT	DISLFD	204	225	CYTOSOLASMIC (POTENTIAL).	
FT	CAROHYD	50	50	POTENTIAL.	
FT	CAROHYD	66	66	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CAROHYD	113	113	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CAROHYD	182	182	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CAROHYD	238	238	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SO	SEQUENCE	575 AA; 64248 MW; 820B9CD576F68B7 CRC64;			
Qy	Query Match	11.5%; Score 164.5; DB 1; Length 575;			
Db	Best Local Similarity	26.7%; Pred. No. 1.8e-07;			
	Matches	74; Conservative 37; Mismatches 89; Indels 77; Gaps 16;			
	6 FLGFLISFLTGVA-GTOSTHSLKRPORVQSRNHNILQWPGRALGNSSVVEYQVK 64				
	8 FLVTTISLSTLEPIAVGT-----ELPSPSYVWFARFQPHILHWKFP--IPNQSSTY---YE 58				

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Oy 65 IMFCSKSSHQKPSGGCMQHISCFPCQRIATLAKYGQROKNKNKEDCMSTOELSCDITSETS 124
Db 59 V-----ALKQXGNSTWMDIHICRQAALSCDITFTL 90
Oy 125 DIEEPYVG---RVRAASAGSYSEMSMT-PRPTPMWETRIKIDPVANNITOV-----NGSLV 175/
    |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 91 DLHRSYGYRARAVRABVDQSYSMNTTETREFT-----VDEVILTVDSYTLKAMDGIITG 144/
Oy 176 ILHAPNLPRYQKEKNNSIETRYELL---RVFLIINNSLEKEQVYGCARAVITEALT- 231/
Db 145 TIHP-----RPTIPPAGEYQVEFDLELVYKI--SIRFSEL-KNAKRVKQETFTL 194/
Oy 232 ----PHSSCYVAETIYOPMLDR---SORSERCVEI 261
Db 195 TVPIGVKRFYKV---LPRLSERLINKAMSEQCLLI 228

RESULT 2
HUMAN STANDARD; PRT; 295 AA.
TF_HUMAN
PI3726:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III)
DE (Thromboplastin) (CD142 antigen).
DE F3.
GN Homo sapiens (Human).
OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=89247359; PubMed=2719931;
RA Mackinn N., Morrissey J.H., Fowler B., Edgington T.S.;
RT "Complete sequence of the human tissue factor gene, a highly
RT regulated cellular receptor that initiates the coagulation protease
RT cascade."
RL Biochemistry 28:1755-1762(1989).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=87260946; PubMed=3037536;
RA Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Guha A.,
RA Krius J., Lin T.C., Nemerson Y., Konigsberg W.H.;
RT "Isolation of cDNA clones coding for human tissue factor: primary
RT structure of the protein and cDNA."
RT Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).
RN 13
RP SEQUENCE FROM N.A.
RX MEDLINE=87244317; PubMed=3297348;
RA Morrissey J.H., Fakhrat H., Edgington T.S.;
RT "Molecular cloning of the cDNA for tissue factor, the cellular
RT receptor for the initiation of the coagulation protease cascade."
RL Cell 50:129-135(1987).
RN 14
RP SEQUENCE FROM N.A.
RX MEDLINE=86050796; PubMed=2823875;
RA Scarpali E.M., Wen D., Broze G.J. Jr., Miletich J.P.,
RA Flandermeyer R.R., Siegel N.R., Sadler J.E.;
RT "Human tissue factor: cDNA sequence and chromosome localization of
RT the gene."
RL Biochemistry 26:5234-5238(1987).
RN 15
RP SEQUENCE FROM N.A.
RX MEDLINE=86100453; PubMed=3424286;
RA Fisher K.L., Gorman C.M., Vehar G.A., O'Brien D.P., Lawn R.M.;
RT "Cloning and expression of human tissue factor cDNA."
RL Thromb. Res. 48:89-99(1987).
RN 16
RP DISULFIDE BONDS, AND PALMITOYLATION.
RX MEDLINE=89000604; PubMed=3166978;
RA Bach R., Konigsberg W.H., Nemerson Y.;

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RT "Human tissue factor contains thioester-linked palmitate and stearate
 on the cytoplasmic half-cysteine";
 RL Biochemistry 27:4227-4231(1988).
 RN
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 33-243.
 RX MEDLINE=94368785; PubMed=8086403;
 RA Muller Y.A., Ullsch M.H., Kelley R.F., de Vos A.M.;
 RT "Structure of the extracellular domain of human tissue factor:
 location of the factor VIIa binding site";
 RL Biochemistry 33:10864-10870(1994).
 RN
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 33-243.
 RX MEDLINE=96190957; PubMed=8609606;
 RA Muller Y.A., Ullsch M.H., de Vos A.M.;
 RT "The crystal structure of the extracellular domain of human tissue
 factor refined to 1.7-A resolution.";
 RL J. Mol. Biol. 256:144-159(1996).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-251 IN COMPLEX WITH EVIIA.
 RX MEDLINE=96175641; PubMed=8598903;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Kongsberg W.H., Nemreson Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor
 VIIa with soluble tissue factor.";
 RL Nature 380:41-46(1996).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 37-242 IN COMPLEX WITH EVIIA.
 RX MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 inhibited with a Bpt mutant";
 RL J. Mol. Biol. 285:2089-2104(1999).
 CC
 CC -I- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
 FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
 NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
 CC
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC
 CC -I- INDUCTION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF
 CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1
 AND TNF, AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND
 VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE
 RESPONSE.
 CC
 CC -I- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
 CC
 CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD142 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd142.htm".
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 DR EMBL: J02931; AAA61150.1; -;
 DR EMBL: M16553; AAA61151.1; -;
 DR EMBL: J02846; AAA61152.1; -;
 DR EMBL: M27436; AAA36734.1; -;
 DR EMBL: A19048; CAA01438.1; -;
 DR PIR: A28320; KFH03.
 DR PIR: A43645; A43645.
 DR PIR: A47574; A47574.
 DR PDB: 1BOY; 10-JUN-96.
 DR PDB: 2HTT; 29-JAN-96.
 DR PDB: 1DAN; 04-SEP-97.
 DR PDB: 1AHW; 19-AUG-98.
 DR PDB: 1TFH; 19-AUG-98.
 DR PDB: 1FAK; 03-DEC-99.
 DR Genew: HGNC:3541; F3.
 DR MIM: 134390; -;
 DR InterPro: IPR000282; Cytok_receptor_2.
 DR InterPro: IPR001187; Tissue_factor.

```

RA Lim J.-K., Langer J.A.;
RT "Cloning and characterization of a bovine alpha interferon receptor.";
RL Biochim. Biophys. Acta 1173:314-319(1993).
CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYRK, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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DR EMBL; X68443; CAA8484.1; -.
DR EMBL; L06320; AAA02571.1; -.
DR PIR; S33770; S33770.
DR PIR; S27387; S27387.
DR InterPro; IPRO00282; Cyto_k_receptor_2.
DR InterPro; IPRO01187; Tissue_factor.
DR Pfam; PF01108; Tissue_fac; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT FT INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT FT CHAIN.
FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
FT TRANSMM 438 458 POTENTIAL.
FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
FT DISULFD 76 84 BY SIMILARITY.
FT DISULFD 199 220 BY SIMILARITY.
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 377 377 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 422 422 F->V (IN REF. 2).
SO SEQUENCE 560 AA; 63818 MW; 66D76B72861E1D11 CRC64;

Query Match 11.1%; Score 158; DB 1; Length 560;
Best Local Similarity 24.1%; Pred. No. 6.7e-07;
Matches 57; Conservative 38; Mismatches 100; Indels 42; Gaps 8;

QY 21 TOSTHESIKPQRVOFOSNFNNIILOMOPGRALTGNSSVYFOYKIMFSCSMKSSHQPSG 80
Db 223 TTERHKVPSPENITQINADNQIVLVKMD---YPYNATFGQWMLRAFPKKIIPGNHSD--- 275
QY 81 CMQHISCFPGCRITLAKGGORMKKNKECKMGTOELISCLLTSETSDIQEPYIGRVARAASAG 140
Db 276 ----- KWKQIPIPCENVSTHCVFPREVVS-RGIYYVRVASNGN 313
QY 141 SYSESWMPREFPMWEETKIDPPVMNIITQV-NGSLIYLIAHNLPYRYOKEKNVSTIEDYE 199
Db 314 GTSMSEKEKENTEMKTITLPPVJLSVKSVTDSDLHSVSGAS-----ESESNMSVNQLYP 367
QY 200 LLYRVFIINNSLEKQKYEGCAHRAVELALEALTPHSYSYCYVAIEIYQPM--RRRSORS 254
Db 368 LIYEIVEMENTSNAERKVLKERTNFI--PPDLKLPLYVCVKA---RALIENDRRNKGS 420

RESULT 4
ID 1105_MOUSE STANDARD; PRT; 349 AA.
CD 061190;
CT 16-OCT-2001 (Ref 40 Created)
```

DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
DN CYtokine receptor class-II CRF2-4).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Eutelestomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97199375; PubMed=9047351;
RA Gibbs V.C., Pennica D.;
RT "CRF2-4: Isolation of cDNA clones encoding the human and mouse
proteins.";
RL Gene 186:97-101(1997).

[2]
CC CHARACTERIZATION,
CX MEDLINE=98130620; PubMed=9463407;
CY Spencer S.D., Di Marco F., Hooley J., Pitts-Meek S., Bauer M.,
CZ Ryan A.M., Sorada B., Gibbs V.C., Aguet M.;
DT "The orphan receptor CRF2-4 is an essential subunit of the interleukin
J receptor."
FT J. Exp. Med. 187:571-578(1998).

-I FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY
CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO
INITIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.

-I SUBCELLULAR LOCATION: Type I membrane protein.

-I SIMILIARITY: CONTAINS 2 FIRONECTIN TYPE III-LIKE DOMAINS.

-I SIMILIARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

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or send an email to license@sib.slb.ch).

EMBL; U53696; AAC53062.1; .
MCD; MG1:109380; 1110rb.
InterPro: IPRO00282; CytoK_receptor_2.
InterPro: IPRO03961; FN_IIT.
SMART; SMART; PNF3.1.
Receptor; Transmembrane; Glycoprotein; Signal.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 19 POTENTIAL.
FT DOMAIN 20 INTERLEUKIN-10 RECEPTOR BETA CHAIN.
FT TRANSMM 221 EXTRACELLULAIR (POTENTIAL).
FT DOMAIN 242 POTENTIAL.
FT DOMAIN 242 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 113 FIBONECTIN TYPE-III.
FT DISULD 66 BY SIMILIARITY.
FT DISULTD 188 BY SIMILIARITY.
FT CARBOHD 49 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHD 102 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHD 161 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHD 199 N-LINKED (GLCNAG...) (POTENTIAL).
FT CARBOHD 199 N-LINKED (GLCNAG...) (POTENTIAL).
SQ SEQUENCE 349 AA; 39774 MW; 58BA4F6B86330A39 CRC64;

Query Match 10.9%; Score 156; DB 1; Length 349;
Best Local Similarity 26.8%; Pred. No. 5.8e-07;
Matches 72; Conservative 30; Mismatches 89; Indels 78; Gaps 13

OY 5 CFLGFLISFLGVAGSTQSHESIKPORAFOPQSRRNHNLLMOV----PERALTGNSSYE 60
DB 4 CVAGWGGEFLVPALCMP-----PEPKRAMSVNFKNLWVEVAPFPNTNL-----FT 53
OY 61 VOYLTFMS---CSMKSSHQSPSGGCWOHITSCEFFPGGRCLATYGGOIRWKNKDCWGTOELS 116
DB 54 AQYESYRSPODHCKRKTAStNQ-----CDF--SLHSKYGD----- 84
OY 117 CDLTSTSIOEPFYRYVAAGAASGSISEWSMPRLFPMWEHTKDPPVMNNITOVNGSLVI 176

[illegible]

Query	Best Local Similarity	10.5%	Score 149.5	DB 1	Length 325
Matches 57	Conservative 32	Mismatches 89	Indels 59	Gaps 8	
QY 30	PQRYQFOSRHNHLIOWPGFALNG--SSYFVQYKIMFSCSMKSSHOKPSCGWQIISC	87			
DB 24	PENVRMMSVYNKKNLQWESPFAKGNLFTAQYLSYRFL	62			
QY 88	NFPGCRILATKGGQKMKKEDCGTQELSCDLISETSDIOEPYGG--RYRASAGSYS	143			
DB 63	-----ODKCMNTTLTECDFSSLSK-----YGDHTLRVRAFFADEHS	98			
QY 144	EMSWTPRTPTPMTWKIKIDPPVNNITQVNGSVLLVLAHNPRLPYRG--KEKNVSIEDYDEL	201			
DB 99	DM-VNIFPCPVDITIIITPBGQVLEVADLSLHMRILAKIENETETTKVKN---YNSWT	153			
QY 202	YRVFIINNSLEKEQYVGAHRAVEIALPHTSSSYCYAAETIYQPMIDRSQSRSEERC	258			
DB 154	YVQYWRKNGDEKFOITPQYDFEV-LRNLEBWTIYCYQVHGOLFIDRRKAGEMWSEPCV	209			
RESULT 7					
TF_BOVIN	STANDARD:	PRT:	292 AA.		
AC P30931					
DT 01-JUL-1993 (Rel. 26, Created)					
DT 01-JUL-1993 (Rel. 26, Last sequence update)					
DT 16-OCT-2001 (Rel. 40, Last annotation update)					
DE Tissue factor precursor (TF) (Coagulation factor III).					
FN F3.					
OS Bos taurus (Bovine).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eularchia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					
OC Bovidae; Bovine; Bos.					
OX NCBI_TaxID=9913;					
RN [1]					
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.					
RC TISSUE=Adrenal gland;					
RC MEDLINE=92109720; PubMed=1764065;					
Takayenoki Y, Muta T, Miyata T, Iwanaga S:					

```

RT      "cDNA and amino acid sequences of bovine tissue factor.";
RL      Bioinformatics. Res. Commun. 181:1145-1150(1991).
CC      - FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC      CIRCULATING FACTOR VII OR VIIA. THE [TF:VITA] COMPLEX ACTIVATES
CC      NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC      PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC      - SUBCELLULAR LOCATION: Type I membrane protein.
CC      - SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
-----
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; S74147; AAB20755.1; -.
DR      PIR; J01319; KFB03.
DR      HSSP; P24055; 1A21.
DR      InterPro; IPRO00282; CytoK_receptor_2.
DR      InterPro; IPRO01187; Tissue_factor.
DR      Pfam; PF01108; Tissue_fac.1
DR      PRINTS; PR00346; TISSUEFACTOR.
DR      PROSITE; PS00621; TISSUE_FACTOR, 1.
KW      Glycoprotein; Blood coagulation; Transmembrane; signal; Lipoprotein;
KM      Palmitate.
FT      SIGNAL          1           35
FT      CHAIN           36         292
FT      DOMAIN          36         248
FT      TRANSSEM        249        271
FT      DOMAIN          272        292
FT      SITE            46         48
FT      CARBOHYD         43         43
FT      CARBOHYD        153        153
FT      CARBOHYD        181        181
FT      DISULFID        81         89
FT      DISULFID        215        238
FT      LIPID           274        274
SQ      SEQUENCE       292 AA; 32475 MW; 5E471D92BFBE163 CRC64;
      Query Match          9.7%; Score 138.5; DB 1; Length 292;
      Best Local Similarity 22.6%; Pred. NO. 1.9e-05;
      Matches 59; Conservative 43; Mismatches 104; Indels 55; Gaps 12
OY      10 LISFLIVAGTQSTHESIKRPOVFOSKNFNIILOWOPGRLITGNSSYYFOYKMFSC 69
OY      21 LEGLVLIGAGAGATTDVVAAYNTWKSNEFTILEMEKPRI---NHHYTVQVIS----- 71
OY      70 SMKSHQKPGCGOWGHICNFPCGRFLAKGQROWKNKKECDMGEOELSCDLTSE-TSDIOE 128
DB      72 -----PRLG--NMKNK--CFYTINCECVPTDEIYKNAVE 101
OY      129 PYRGHVRAASAGSYSE----WSMTPRFTPMWEETKI-DPPVANITOVNGSLVLIHPNL 182
DB      102 TYLARVLSPADYTSSTVEPPTNSPEFPYLETNIGOPTIOSFEQVGTKLVNYVDART 161
OY      183 PYRYKKENVSIEDYY--ELLARYVFINLSLEKQKVYGSAHR-AVEIALPHSSYC-- 237
DB      162 LVV-ANSAFLSRDVPFGKDLNTLLYLWKRASSTGGKKATNTNIGFLIDD:-KGENTCFH 217
OY      238 VVAEIYOPMLDRRSORSEERC 258
DB      218 VQAVTLSTRVNQKSPESPICK 238
RESULT 8
TF_CAVPO STANDARD; PRT; 289 AA.
AC 09JUL8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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QY	168	--QVNGSLIIV--LHAPNLPY	184
DE	16-OCN-2001 (Rel. 40, Last annotation update)		
DE	Tissue precursor (TF) (Coagulation factor III).		
OS	F3.		
OS	Cavia porcellus (Guinea pig).		
OC	Eukaryota; Metazoa; Chordata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.		
OX	NCBI_TaxID=10141;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
FX	MEDLINE=20206020; PubMed=10744153;		
RA	Shi R.-J., Li W.-Z., Marder V.J., Sporn L.A.;		
RT	"Cloning of guinea pig tissue factor cDNA: comparison of primary		
RT	structure among six mammalian species."		
RL	Thromb. Haemost. 83:445-461(2000).		
CC	-1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH		
CC	CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES		
CC	FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN		
CC	NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND		
CC	PROPAOGATION OF THE COAGULATION PROTEASE CASCADE.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/).		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; AF131949; AAF36523.1; -		
DR	HSSP; P13726; 1TFH.		
DR	InterPro; IPR000282; Cytok_receptor_2.		
DR	InterPro; IPR001187; Tissue_factor.		
DR	Pfam; PF01108; Tissue_fac; 1.		
DR	PRINTS; PR00346; TISSUEFACTOR.		
DR	PROSITE; PS00621; TISSUE_FACTOR; FALSE NEG.		
KW	Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;		
KW	Palmitate.		
FT	SIGNAL	1	32
FT	CHAIN	33	289
FT	DOMAIN	33	247
FT	TRANSMEM	248	268
FT	DOMAIN	269	289
FT	SITE	44	46
FT	SITE	75	77
FT	CARBOHYD	41	41
FT	CARBOHYD	111	111
FT	CARBOHYD	151	151
FT	CARBOHYD	164	164
FT	DISULFD	79	87
FT	DISULFD	213	236
FT	LIPID	271	271
FT	SEQUENCE	289 AA; 32456 MW; 7AB97F8F58199FBI CRC64;	
QY	Query Match	9.6%;	Score 136.5; DB 1; Length 289;
QY	Best Local Similarity	24.9%;	Pred. No. 2.9e-05;
QY	Matches 50; Conservative 32; Mismatches 52; Indels 67; Gaps 11.		
QY	10 LISFLITGVAGTQSHESIKKPORVQFOSNFINILIQMGKRLTNGSSYYFYQKIMFSC 69		
QY	21 ILGWLVQVAGAGGI--PKVPYNLLTWKSTNFETLLEWPKPI---NNVYVQ---IST 70		
QY	70 SAKSSHOKPSGQMOHISCNFPCGCRTLAKYGGQRMKNKEDCMGCTOELSCDLTSETS-DIOE 128		
QY	71 ALPD-----WKSL-----CFSLTATECDLTSEMANVQO 99		
QY	129 PYYGRVRAA---SAGSYSE--WSMIDRETPMWETKIDP-----VNIT----- 167		
QY	100 TILARIYSILLPNSTGFLIEDAVYNSNPFYQVETNIGQPIESFKLVGTRKLVNTVADTQI 159		
QY	168 --QVNGSLIIV--LHAPNLPY 184		

FT DISULFID 199 220 BY SIMILARITY.
 FT MOD_RES 466 466 PHOSPHORYLATION (BY TYK2) (PROBABLE).
 FT MOD_RES 481 481 PHOSPHORYLATION (BY TYK2) (PROBABLE).
 FT CARBOHYD 50 50 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 58 58 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 81 81 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 110 110 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 254 254 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 313 313 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 314 314 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 376 376 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 416 416 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT VARIANT 168 168 L -> V.
 FT /FTID=VAR.002717.
 FT CONFLICT 17 17 G -> A (IN REF. 2).
 FT SEQUENCE 557 AA: 63525 MW: 0f6744c8a1adbef73 CRC64:
 Query Match 9.6%; Score 136.5; DB 1; Length 557;
 Best Local Similarity 20.8%; Pred. No. 6.3e-05;
 Matches 54; Conservative 39; Mismatches 115; Indels 51; Gaps 7.
 QY 2 PKHCLGLGFLIFLTVAGACTOSTHSLKQRYQVQFSRNFHNLQMPGHALTGSSVYFV 61
 DB 217 PVHCL-----KTYVENLEPPENIEVSQUNQVYLKMD---YYANMTFQV 259
 QY 62 QYKIFSCSMKSHQKPSGCMQHISCNPGCGTTLAKYGRQKKNKEDCMGTDELSCDLTS 121
 DB 260 QWLAHFLKRNQGNH-----LYKKWQIPDCENVYTKQCVFQ 295
 QY 122 ETSIDQIEPYGRVRAASAGSYSEMSMTPRFTPMWETKIDIPVMTITVOVGSLLVILHAVN 181
 DB 296 NVQV-KGTYLLRVQASDGNNTSFMSEELIKFDEIQAFLLPVPYFNRSLSDSHYIITGAP- 353
 QY 182 LPYRQKKRNVSIEDYVLLRVFTIINNSLEKQKQVYGAAHRAVEIEALTPHSSCYAAE 241
 DB 354 -----KQSGNPNVIOQDYPLIYEIIEMWENTSNAERKIIIE-KKTDVTVPNLKLPIYCVVAR 407
 QY 242 IY-QPMLDRRSQRSEERC 258
 DB 408 AHYMDERLKNSSVPSDAYC 426
 RESULT 10
 INRL-SHEEP STANDARD; PRT; 560 AA.
 AC Q28589; Q95206;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-BEC)
 DE (Interferon alpha/beta receptor-1).
 GN IFNARI OR IFNAR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OC NCBL_TaxID=9940;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endometrium;
 RX MEDLINE=97135690; PubMed=8981227;
 RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
 RT "Structure of an ovine interferon receptor and its expression in
 endometrium.";
 RT J. Mol. Endocrinol. 17:207-215(1996).
 RL [2]
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Endometrium;
 RX MEDLINE=98006426; PubMed=9348203;
 RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;

QY 170 NGSLLVILHAAPNLPYRYQKKNVSIEDYVLLRYVFIINNSLEKEQVYEGARAVEIEA 229
 DB 139 DKALIVHISPPG-----QDGNMMALEKPSFSYTIIRIMQK--SSDKKTINSTYVYKPIE 191
 QY 230 LTPHSSYCVVAETIOPMLDRSQRSERCV 259
 DB 192 LLPETTYCLEVKAHPISLKHNSYSTVOCI 221

RESULT 12

TF_RABIT	STANDARD	PRT	292 AA
ID	TF_RABIT		
AC	P24055		
DT	01-MAR-1992 (Rel. 21, Created)		
DT	01-MAR-1992 (Rel. 21, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Tissue factor precursor (TF) (Coagulation factor III).		
GN	F3.		
OR	Oryctolagus cuniculus (Rabbit).		
RA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Heart;		
RC	MDLINE=91200676; PubMed=1840552;		
RA	Andrews B.S., Rehmanulla A., Fowler B.J., Edgington T.S., Mackman N.		
RT	"Conservation of tissue factor primary sequence among three mammalian species";		
RL	Gene 98:265-269(1991).		
RN	[2]		
RP	SEQUENCE OF 33-292 FROM N.A.		
RC	STRAIN-New Zealand white; TISSUE-Brain;		
RC	MDLINE=92081032; PubMed=1746002;		
RA	Pawashe A., Ezekowitz M., Lin T.C., Horton R., Bach R., Konigsberg W.		
RT	"Molecular cloning, characterization and expression of cDNA for rabbit brain tissue factor";		
RL	Thromb. Haemost. 66:315-320(1991).		
RN	[3]		
RP	X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 36-240.		
RC	MDLINE=98266351; PubMed=9605315.		
RA	Muller Y.A., Kelley R.F., de Vos A.M.;		
RT	"Hinge bending within the cytokine receptor superfamily revealed by the 2.4 A crystal structure of the extracellular domain of rabbit tissue factor";		
RL	Protein Sci. 7:1106-1115(1998).		
CC	-1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH CIRCULATING FACTOR VIT OR VITA. THE (TF:VITA) COMPLEX ACTIVATES FACTORS IX OR X BY SPECIFIC LIMITED PROTOCLYSIS. TF PLAYS A ROLE IN NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND PROPAGATION OF THE COAGULATION PROTEASE CASCADE.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-1- TISSUE SPECIFICITY: BRAIN, HEART.		
CC	-1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.		
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CC	EMBL; M55390; AAA63469.1; -		
DR	EMBL; X53521; CAA37597.1; -		
DR	PIR; J00441; KFRB3.		
DR	PIR; S23681; S23681.		
DR	PDB; 1A21; 27-MAY-98.		
DR	InterPro; IPR000282; Cytok_receptor_2.		
DR	InterPro; IPR001187; Tissue_factor.		
DR	Pfam; PF01108; Tissue_fac.1.		
DR	PRINTS; PR00346; TISSUEFACTOR.		

DR PROSITE; PS00621; TISSUE_FACTOR; 1.
 KW Glycoprotein; Blood coagulation; Transmembrane; signal; Lipoprotein;
 KM Palmitate; 3d-structure.

FT	SIGNAL	1	32	TISSUE FACTOR.
FT <td>CHAIN</td> <td>33</td> <td>292</td> <td>EXTRACELLULAR (POTENTIAL).</td>	CHAIN	33	292	EXTRACELLULAR (POTENTIAL).
FT <td>DOMAIN</td> <td>33</td> <td>250</td> <td>POTENTIAL.</td>	DOMAIN	33	250	POTENTIAL.
FT <td>TRANSMEM</td> <td>251</td> <td>271</td> <td>CYTOPLASMIC (POTENTIAL).</td>	TRANSMEM	251	271	CYTOPLASMIC (POTENTIAL).
FT <td>DOMAIN</td> <td>272</td> <td>292</td> <td>WKS MOTIF.</td>	DOMAIN	272	292	WKS MOTIF.
FT <td>SITE</td> <td>44</td> <td>46</td> <td>WKS MOTIF.</td>	SITE	44	46	WKS MOTIF.
FT <td>SITE</td> <td>75</td> <td>77</td> <td>WKS MOTIF.</td>	SITE	75	77	WKS MOTIF.
FT <td>CARBOHYD</td> <td>41</td> <td>41</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <td>CARBOHYD</td> <td>114</td> <td>114</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	114	114	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <td>CARBOHYD</td> <td>154</td> <td>154</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <td>CARBOHYD</td> <td>167</td> <td>167</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	167	167	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <td>CARBOHYD</td> <td>182</td> <td>182</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	182	182	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <td>DISULFID</td> <td>79</td> <td>87</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	DISULFID	79	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <td>DISULFID</td> <td>216</td> <td>239</td> <td></td>	DISULFID	216	239	
FT <td>LIPID</td> <td>274</td> <td>274</td> <td></td>	LIPID	274	274	
SO	SEQUENCE	292 AA;	32738 MW;	PALMITATE (BY SIMILARITY). 4860A1CADBACCF71 CRC64;

Query Match 9.3%; Score 132.5; DB: 1; Length 292;
 Best Local Similarity 22.2%; Pred. No. 6.7e-05;
 Matches 62; Conservative 39; Mismatches 89; Indels 89; Gaps 13;

QY 10 LISFELTGAVAGTOSTHESLIKPORVQFOSRNFHILOMOPGRALTGSSVYFYQKIMFSC 69
 DB 21 LIGWLLAQAARAAT--TGRAVNLTKWSTNFKTILEMP-----KSIDHV-YTVQIST 70
 QY 70 SMSSHOKPSCGOWHISCNPFGRCTLAKYGGQKKNKEDCWGTOELSCDLTSE-TSDIQE 128
 DB 71 RLEN-----WKSK--CFETAFETCDLDEYVKKVGGQ 99

QY 129 PYGGRV-----RASAGSYSE--WSMIRPTPMWETKIDPV-----NAITOVN 170
 DB 100 TYARAVLSTPARNGNTGTFPEPPFRNSPEFTPLDNLGPTQISFQGVETKRLVYQD 159
 QY 171 GSLVILHAAPNLPYR--YQKKNVSIEDYVLLRYVFIINNSLEKEQVYEGARAVEIEA 221
 DB 160 ARTLVRRNGTFLSLRAVFGDLN-----YLLYWRASSSTGKATATNTNFEFLIDVDAGE 213

QY 222 HRAVEIALTPHSSYCVVAETIOPMLDRSQRSERCVE 260
 DB 214 NCFYSQAVVIPSR-----KKKORSPESLTE 238

RESULT 13.

TF_RAT	STANDARD	PRT	295 AA
ID	TF_RAT		
AC	P42533;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Tissue factor precursor (TF) (Coagulation factor III).		
GN	CFS.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Sprague-Dawley;		
RC	MDLINE=97108126; PubMed=8950776;		
RA	Taby O., Rosenfield C.L., Bogdanov V., Nemerson Y., Taubman M.B.;		
RT	"Cloning of the rat tissue factor cDNA and promoter: identification of a serum-response region";		
RL	Thromb. Haemost. 76:697-702(1996).		
CC	-1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH CIRCULATING FACTOR VIT OR VITA. THE (TF:VITA) COMPLEX ACTIVATES FACTORS IX OR X BY SPECIFIC LIMITED PROTOCLYSIS. TF PLAYS A ROLE IN NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND PROPAGATION OF THE COAGULATION PROTEASE CASCADE.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.		

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 CC or send an email to license@isb-sib.ch).

CC EMBL: 007619; AAA16966.1; -.
 DR HSSP: P13726; IFAK.
 DR InterPro: IPR000282; Cytok_receptor_2.
 DR InterPro: IPR001187; Tissue_factor.
 DR Pfam: PF01108; Tissue_fac1.
 DR PRINTS: PR00346; TISSUEFACTOR.
 DR PROSITE: PS00621; TISSUE_FACTOR; 1.
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
 KW Palmitate.

FT SIGNAL 1 28
 FT CHAIN 29 295
 FT DOMAIN 29 252
 FT TRANSMEM 253 275
 FT DOMAIN 276 295
 FT SITE 246 248
 FT CARBOHYD 38 38
 FT CARBOHYD 58 58
 FT CARBOHYD 95 95
 FT CARBOHYD 109 109
 FT CARBOHYD 170 170
 FT CARBOHYD 201 201
 FT DISULFID 76 84
 FT DISULFID 219 242
 FT LIPID 276 276
 FT SEQUENCE 295 AA; 33443 MW; E64C15B4B3628D48 CRC64;

Query Match 9.0%; Score 128.5; DB 1; Length 295;
 Best local Similarity 22.9%; Pred. No. 0.00016;
 Matches 66; Conservative 37; Mismatches 92; Indels 93; Gaps 14;

QY 6 FLGLFLISFLITGVAGTOSTHESLKPQRYOFOSRNHNILQMPGALNGSSVYFYQYKI 65
 DB 17 FLGLLIQVAVG-AGTPRG-----KAFNLTWISTDKTILEWQP---KPTNYTYTVQ--- 64
 QY 66 MFSCSMKSSHQKPGSCQWQHISCNFPGCRITLAKYGGORWKNKEDCGTQELSDLTSE-TS 124
 DB 65 ----ISDS-----RNMKNK--CGTDTDEDDLDELIVK 92
 QY 125 DIOEPYGRV-----RAASAGSYSE--WSMTPTPTPMTETKIDPPVMTITQVN 170
 DB 93 DVNMTYEARVLVSPWRNSTHGKELFTGHGEPPPTNARKFLPYRDTKIGQPVQIKYEKG 152
 QY 171 GLLVLIHAAPMLPRYQKEKVNISIEDIYELLYR--VFIIINSLKEQKYBECAHR--AV 225
 DB 153 GTKL-----KVTYKDSFTLVKNGTFLTLRVFVNDIGLYITLRKDSST 196
 QY 226 EIEALTPHS-----SYCVAAE--IYQPMIDRRSQRSEECVE 260
 DB 197 GRKTNTHITNEFLIDVEKGVSYCFPAQAVIFSRKTNHKSPESTICTE 244

RESULT 14
 TF_MOUSE STANDARD: PRT: 294 AA.
 AC P20352;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tissue factor precursor (TF) (Coagulation factor III).
 GN F3 OR CF3 OR CF-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91093171; PubMed-1985911;
 RA Ranganathan G., Blattl S.P., Sudramaniam M., Fass D.N., Mainle N.J.,
 RA Getz M.J.;
 RT "Cloning of murine tissue factor and regulation of gene expression by
 RT transforming growth factor type beta 1.";
 RL J. Biol. Chem. 266:496-501(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Hartzell S., Ryder K., Lanahan A., Lau L.F., Nathans D.;
 RT "A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a
 RT protein homologous to human tissue factor.";
 RL Mol. Cell. Biol. 9:2567-2573(1989).
 CC -I- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CC CIRCULATING FACTOR VII OR VIIA. THE (TF:VIIA) COMPLEX ACTIVATES
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 CC PROPAagation OF THE COAGULATION PROTEASE CASCADE.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
 CC -----
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DR EMBL: M57896; AAA63400.1; -.
 DR EMBL: M26071; AAA40414.1; -.
 DR PIR: A32318; RFMS3.
 DR HSSP: P13726; IFAK.
 DR MGD: MGI:88381; F3.
 DR InterPro: IPR000282; Cytok_receptor_2.
 DR InterPro: IPR001187; Tissue_factor.
 DR Pfam: PF01108; Tissue_fac1.
 DR PRINTS: PR00346; TISSUEFACTOR.
 DR PROSITE: PS00621; TISSUE_FACTOR; 1.
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
 KW Palmitate.

FT SIGNAL 1 28
 FT CHAIN 29 294
 FT DOMAIN 29 251
 FT TRANSMEM 252 274
 FT DOMAIN 275 294
 FT SITE 245 247
 FT CARBOHYD 37 37
 FT CARBOHYD 57 57
 FT CARBOHYD 169 169
 FT CARBOHYD 200 200
 FT DISULFID 75 83
 FT DISULFID 218 241
 FT LIPID 275 275
 FT SEQUENCE 294 AA; 32935 MW; A306101293C31FA0 CRC64;

Query Match 8.7%; Score 124; DB 1; Length 294;
 Best local Similarity 22.7%; Pred. No. 0.00041;
 Matches 64; Conservative 36; Mismatches 100; Indels 82; Gaps 13;

QY 6 FLGLFLISFLITGVAGTOSTHESLKPQRYOFOSRNHNILQMPGALNGSSVYFYQYKI 65
 DB 17 FLGLLIQVAVG-AGTPE-----KAFNLTWISTDKTILEWQP---KPTNYTYTVQ--- 63
 QY 66 MFSCSMKSSHQKPGSCQWQHISCNFPGCRITLAKYGGORWKNKEDCGTQELSDLTSE-TS 124
 DB 64 ----ISDS-----RNMKNK--CFSTDTDEDDLDELIVK 91
 QY 125 DIOEPYGRVRAASA-----GSEYSMTPTPTPMTETKIDPPV----- 163

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Db 92 DVTWAYEAKVLSVBRNSVHGDDQVLIHGEEPPPTNAPKFLPYRDTNIGQVYIQOEOD 151
QY 164 ---NNIQVNSGLVLIHAPNLPYVQKEKNVSIIDYELLYRVPIINSLKEQKVEYG 220
Db 152 GRKLNVAVKDSLTLRKNGTFLTRQVFGKDLG---YIIYRK---GSSSTGKKTITWT 204
QY 221 AHRAVEIALTPHSSYC--VVAETIYQPMIDRRSQRSEECVE 260
Db 205 NEFSIDVE---EGVSYCFVQAMIFSRKTNONSPOSSIVCTE 243

RESULT 15
ID INGR_HUMAN STANDARD; PRT; 489 AA.
AC P15260;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
Interferon gamma receptor alpha chain precursor (CDw119).
iFNGRL.
Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89003065; PubMed=2971451;
RA Aguet M., Dembic Z., Merlin G.;
RT "Molecular cloning and expression of the human interferon-gamma
RT receptor.",
RT Cell 55:273-280(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Phillimore B.;
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=prostate;
RA Strausberg R.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
RA MEDLINE=93183911; PubMed=8443182;
RA Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Garotta G.;
RT "Alignment of disulfide bonds of the extracellular domain of the
RT interferon gamma receptor and investigation of their role in
RT biological activity.",
RT Biochemistry 32:2423-2430(1993).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RA MEDLINE=95342235; PubMed=7617032;
RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lunn C.A.,
RA Zavadny P.J., Narula S.K.;
RT "Crystal structure of a complex between interferon-gamma and its
RT soluble high-affinity receptor.",
RT Nature 376:230-235(1995).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 IN COMPLEX WITH
RP ANTI BODY.
RA MEDLINE=96035727; PubMed=9367779;
RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA Winkler F.K., Robinson J.A.;
RT "Neutralizing epitopes on the extracellular interferon gamma receptor
RT and X-ray crystal structure of the A6 fab-IFNgamma-108 complex.",
RT J. Mol. Biol. 273:882-897(1997).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF COMPLEX WITH ING.
RA MEDLINE=20444407; PubMed=10986460;
RA Thiel D.J., Le Du M.-H., Walter R.L., D'Arcy A., Chene C.,
RA Fountoulakis M., Garotta G., Winkler F.K., Falick S.E.;
RT "Observation of an unexpected third receptor molecule in the crystal

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RT structure of human interferon-gamma receptor complex.",
RL Structure 8:927-936(2000).
CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
CC INTERFERON-GAMMA DIMER.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CDw119 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw119.htm".
CC
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DR EMBL; J03143; AA52731.1; -
DR EMBL; AL050337; CAB53062.1; -
DR EMBL; BC005333; AAH05333.1; -
DR PIR; A31555; A31555.
DR PDB; LURH; 25-MAR-98.
DR PDB; IFG9; 11-AUG-00.
DR GlycoSuiteDB; P15260; -
DR Genew; HGNC:5439; IFNGRL.
DR MIM; 107470; -
DR MIM; 209950; -
DR InterPro; IPR000282; Cytok_receptor_2.
DR Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Immunoglobulin domain; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 489
FT DOMAIN 18 245 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
FT TRANSMEM 246 266 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).
FT DISULFID 77 85
FT DISULFID 122 167
FT DISULFID 195 200
FT DISULFID 214 235
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 489 AA; 54404 MW; DCF9E574DBF47400 CRC64;

Query Match 8.6%; Score 122.5; DB 1; Length 489;
Best Local Similarity 20.1%; Pred. No. 0.001;
Matches 56; Conservative 49; Mismatches 103; Indels 71; Gaps 10;

QY 9 FLISFLFLGVA-----GTSTHSL--KPORVQFSRNFHNLQWOPGRALTGNSVYFVQ 62
Db 5 FLPLVMGVSRRAEMGTADLGPSSVPTNTVIESYNMNPVIYV-----E 49
QY 63 YKIM-----FSCSMKSHQKPSGCGWQHTSCNPPGRTILAKYQGRQKKNKEDCGTQELSC 117
Db 50 YQIMPQVPTFVEYKN-----YGVKNSWIDACINISHHYC 85
QY 118 DLTSETSDIQEPYGRVRAASAGSYSEWSMPTPTPMWETKIDPPVMNTQVNGSLVLT 177
Db 86 NISHDVDDPSNSLWVRVAVRGOKESAAYAKSBEFVACDCKGPKKIDIRKEKQIMDI 145
QY 178 HAPNLPYVQKEKNVSIIDY-----YELLYRVPIINSLKEQKVE-----GAH 222
Db 146 FHSV-FVNGDEDEV--DVDEFTTCYIRVNVYVYRMNGSEYQKILTKEDDCEIQCO 201
QY 223 RAVEIEALTPHSSYCAVAETIYQPMIDRRSQRSEECVEI 261
Db 202 LAIPVSSL--NSQYCAAGCVLHWGVTTEKSKVCYCIIT 238

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Mon Dec 23 08:50:22 2002

us-09-964-994-2.rsp

Page 12

Search completed: December 22, 2002, 10:11:37
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: December 22, 2002, 10:09:37 ; Search time 26 Seconds
(Without alignments)
296.493 Million cell updates/sec

Title: US-09-964-994-2

Perfect score: 1427
Sequence: 1 MKHCFGLGFLISFLTGAVG.....YQPLDRRSORSERCVEIP 262

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCRTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	311	21.8	221	2	US-08-943-087-52
2	310	21.7	221	2	US-08-943-087-50
3	310	21.7	221	2	US-08-943-087-56
4	310	21.7	553	2	US-08-943-087-2
5	310	21.7	553	2	US-08-943-087-14
6	310	21.7	553	2	US-08-943-087-16
7	310	21.7	553	2	US-08-943-087-18
8	310	21.7	553	2	US-08-943-087-20
9	310	21.7	553	2	US-08-943-087-22
10	310	21.7	553	2	US-08-943-087-24
11	310	21.7	553	2	US-08-943-087-26
12	310	21.7	553	2	US-08-943-087-28
13	310	21.7	553	2	US-08-943-087-30
14	310	21.7	553	2	US-08-943-087-32
15	310	21.7	553	2	US-08-943-087-34
16	310	21.7	553	2	US-08-943-087-36
17	310	21.7	553	2	US-08-943-087-38
18	310	21.7	553	2	US-08-943-087-40
19	310	21.7	553	2	US-08-943-087-42
20	310	21.7	553	2	US-08-943-087-44
21	310	21.7	553	2	US-08-943-087-46
22	310	21.7	553	2	US-08-943-087-48
23	308	21.6	221	2	US-08-943-087-54
24	303	21.2	221	2	US-08-943-087-58
25	299	21.0	221	2	US-08-943-087-60
26	240	16.8	574	2	US-08-906-713-2
27	164.5	11.5	575	1	US-08-424-788-2

28	164.5	11.5	575	1	US-08-110-683-4	Sequence 4, Appl1
29	164.5	11.5	575	2	US-08-477-166-4	Sequence 4, Appl1
30	164.5	11.5	575	2	US-08-472-097-4	Sequence 4, Appl1
31	164.5	11.5	575	4	US-09-439-672-4	Sequence 4, Appl1
32	164.5	11.5	575	5	PCT-US93-11638-4	Sequence 4, Appl1
33	163	11.4	251	1	US-07-882-202A-2	Sequence 2, Appl1
34	163	11.4	251	1	US-07-683-682B-4	Sequence 4, Appl1
35	163	11.4	251	1	US-08-021-615A-2	Sequence 2, Appl1
36	163	11.4	251	1	US-08-321-777-2	Sequence 2, Appl1
37	163	11.4	251	1	US-08-463-931-6	Sequence 6, Appl1
38	163	11.4	251	1	US-08-464-237A-4	Sequence 4, Appl1
39	163	11.4	251	5	PCT-US92-02898A-4	Sequence 4, Appl1
40	163	11.4	251	1	PCT-US93-04493-2	Sequence 2, Appl1
41	163	11.4	295	1	US-08-463-931-2	Sequence 2, Appl1
42	163	11.4	295	4	US-08-372-887-20	Sequence 20, Appl1
43	163	11.4	295	4	US-09-224-048A-4	Sequence 4, Appl1
44	162	11.4	559	1	US-08-424-788-3	Sequence 3, Appl1
45	155	10.9	227	4	US-08-871-572B-14	Sequence 14, Appl1

ALIGNMENTS

RESULT 1
US-08-943-087-52
; Sequence 52, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 221 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-52

Query Match	21.8%;	Score 311;	DB 2;	Length 221;
Best Local Similarity	32.0%;	Pred. No. 1.3e-27;		
Matches	74;	Conservative	33;	Mismatches 90;
			Indels	34;
			Gaps	3

[illegible]

Matches	74;	Conservative	33;	Mismatches	90;	Indels	34;	Gaps	37;
---------	-----	--------------	-----	------------	-----	--------	-----	------	-----

QY	29	KPOKVCOSNRNHHIIIMOGFRALTGSSVYFOYKIMFGSCMKS	SHOKPSGOWHISCN	88
Db	10	KPANIITLISIMKAVLOWMPREGLOGVKITYTOYFI	-----	46
QY	89	FPFGRTLAKYGOBOMKNEKEDOWGTQELSCDUTSETSDIQE	PIYGRVRAASAGSIEMSMIT	148
Db	47	-----YGOKWILKSECRINIRNTQCDLSAETSDPYE	QYQYAAKVAINGTCKSAES	97
QY	149	PRTPPMHETKIDPRVMMITQVNGSLVILHAPNLPYKQEKUN	SIEDDY-ELLYRFII	207
Db	98	GRFPRFLETOIGPREVALITJDEKISIVYLTAPEKWKNP	EDLPYSMOQIYNLKNYSVL	157
QY	208	NNSLEKQKVEGAHRAVAIEFALPRHSSCYVAEIIYO	PMIDRPSQRSEKRC	258
Db	158	NTKSNRRTWSQCVTNHTLV-LTWLEPNLLCYCHVESFV	GPBRRAQPSSEKQC	207

QY 29 KPOAVQFOSRNFHNLQWOPGRALITGNSVYFVQYKIMFSCMSKSSHQKPSGCMQHISCN 88
Db 10 KPAITFLSLIMKKNVLTQWTPPEGLOGVAKVYTVQYFI----- 46
QY 89 FPGCRITLAKYQOROMKKNKEDCWGTQELSDLTSETSDIOEPYGRVRAASAGSYSTEMT 148
Db 47 -----YGOKKWLKNSCRNINRTYCDLSAETSDEHYAKVKAIMGCKSKMAES 97
QY 149 PRFTPMWETKIDPPVNMITGVNSLVLTLHAPNLPRYQKEKNVSIEDYY-ELLYRVFII 207
Db 98 GREYPLETQIGPEVALITSEKISIVYLAPEKWKRNPEDLPVSMQIYSNLKYNVSVL 157
QY 208 NNSLEKQKVEGAHRAVEIALTPHSSYCVVAETIYOPMLDRSORSEREC 258
Db 158 NTKSNRTWSOCVTNHTLY-LTWLEPNTLYCVHVSFVGPBRRAQPSERKQC 207

RESULT 4
US-08-943-087-2

Sequence 2, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Fairah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-2

Query Match 21.7%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 7.2e-27;

Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;
QY 29 KPOAVQFOSRNFHNLQWOPGRALITGNSVYFVQYKIMFSCMSKSSHQKPSGCMQHISCN 88
Db 10 KPAITFLSLIMKKNVLTQWTPPEGLOGVAKVYTVQYFI----- 46

Db 39 KPAITFLSLIMKKNVLTQWTPPEGLOGVAKVYTVQYFI----- 75
QY 89 FPGCRITLAKYQOROMKKNKEDCWGTQELSDLTSETSDIOEPYGRVRAASAGSYSTEMT 148
Db 76 -----YGOKKWLKNSCRNINRTYCDLSAETSDEHYAKVKAIMGCKSKMAES 126
QY 149 PRFTPMWETKIDPPVNMITGVNSLVLTLHAPNLPRYQKEKNVSIEDYY-ELLYRVFII 207
Db 127 GREYPLETQIGPEVALITSEKISIVYLAPEKWKRNPEDLPVSMQIYSNLKYNVSVL 186
QY 208 NNSLEKQKVEGAHRAVEIALTPHSSYCVVAETIYOPMLDRSORSEREC 258
Db 187 NTKSNRTWSOCVTNHTLY-LTWLEPNTLYCVHVSFVGPBRRAQPSERKQC 236

RESULT 5
US-08-943-087-14

Sequence 14, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Fairah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-14

Query Match 21.7%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 7.2e-27;

Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;
QY 29 KPOAVQFOSRNFHNLQWOPGRALITGNSVYFVQYKIMFSCMSKSSHQKPSGCMQHISCN 88
Db 39 KPAITFLSLIMKKNVLTQWTPPEGLOGVAKVYTVQYFI----- 75

QY	89	FPCRLIAKGGOMKNKEOCMTQELSDLTSETSDIDPEYGGRYAANASGYSIEMSM	148
Db	76	-----YGOKMKLMSCECRNINRTQSLAETSIDYEYQYAKAKALMGTCRMAES	126
QY	149	PRFTPMWERTIIDPEVNMIIQVNSLSVLIILAPMLPYRQEKVNSIEDDY-ELLYRFIL	207
Db	127	GREYPELETIIGPEVALTTDEKSSISVYLAPEKMKKNPDELPKSMQIYSNLKYNVSVL	186
QY	208	NNSLERQKYEGAGHRAVETALTPHSSCYVAEAIQYPMIDRRSORSEERC	258
Db	187	NTKSNRKWSOCVTNNHLY-LTWLEPNLLCYVHNESFYGPGRARRQSEKOC	236

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1      RESULT 6
2      US-08-943-087-16
3      ; Sequence 16, Application US/08943087
4      ; Patent No. 594511
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: Lok, Si
9      ; APPLICANT: Kho, Choon J.
10     ; APPLICANT: Jelmeberg, Anna C.
11     ; APPLICANT: Adams, Robyn L.
12     ; APPLICANT: Whitmore, Theodore E.
13     ; APPLICANT: Farrah, Theresa M.
14     ; TITLE OF INVENTION: CYTOKINE RECEPTOR
15     ; NUMBER OF SEQUENCES: 60
16     ; CORRESPONDENCE ADDRESS:
17     ; ADDRESSEE: Zymogenetics, Inc.
18     ; STREET: 1201 Eastlake Avenue East
19     ; CITY: Seattle
20     ; STATE: WA
21     ; COUNTRY: USA
22     ; ZIP: 98102
23     ;
24     ; COMPUTER READABLE FORM:
25     ; MEDIUM TYPE: Diskette
26     ; COMPUTER: IBM compatible
27     ; OPERATING SYSTEM: DOS
28     ; SOFTWARE: FASTSEQ for Windows Version 2.0
29     ;
30     ; CURRENT APPLICATION DATA:
31     ; APPLICATION NUMBER: US/08/943,087
32     ; FILING DATE:
33     ; CLASSIFICATION: 536
34     ; PRIOR APPLICATION DATA:
35     ; APPLICATION NUMBER: 08/803,305
36     ; FILING DATE: 20-FEB-1997
37     ; ATTORNEY/AGENT INFORMATION:
38     ; NAME: Lunn, Paul G
39     ; REGISTRATION NUMBER: 32,743
40     ; REFERENCE/DOCKET NUMBER: 96-24C1
41     ; TELECOMMUNICATION INFORMATION:
42     ; TELEPHONE: 206-442-6627
43     ; TELEFAX: 206-442-6678
44     ;
45     ; TEXES:
46     ; INFORMATION FOR SEQ ID NO: 16:
47     ;
48     ; SEQUENCE CHARACTERISTICS:
49     ;
50     ; LENGTH: 553 amino acids
51     ; TYPE: amino acid
52     ; STRANDEDNESS: single
53     ; TOPOLOGY: linear
54     ;
55     ; MOLECULE TYPE: protein
56     ; FRAGMENT TYPE: internal
57     ;
58     ; US-08-943-087-16

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Query Match	21.7%	Score 310;	DB 2;	Length 553;
Best Local Similarity	32.0%	Pred. No. 7.2e-27;		
Matches 74; Conservative	35;	Mismatches 90;	Indels 34;	Gaps 3

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QY      29 KQQRQFQSRNHNHLNMQPGALITGNSYVEYQKIFSCSMKSHQKPGCQWQHISCN 88
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Db      39 KANITFLFLINKKINVLNMQPREGLOGVRYTYVOYFI-----75
QY      89 FPGCKTLAKYGRQKKNEKDCWGTQLSCDLTSEFSQDIEPYRGVRAASGYSSEKSMT 148
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 76 -----YGGKKKLINKSCSRNINRYODLSAETSDIEHYQYAKKAIIMGTGCSKWAES 126

QY 149 PRFPMTWEKLTIDPPVANNITQVNSLLYIIHAAPLPRYKOEKKNVSTJEDY -ELLYRVFTI 207

Db 127 GRFPFETETQGPPEVALITDEKSIISVYLAPEKKRNRPEDLEVSQOQIISNLYKYNVSL 186

QY 208 NNSLLEKQKYEGCAHRAVETLEALTPHSYCYVAALITQPMIDRSQSEKCC 258

Db 187 NTKSNRWSOCVATHTLTYLTWLEPNLYCVHVESFQGPGRKAOSEKCC 236

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Query Match	21.7%	Score 310;	DB 2;	Length 553;
Best Local Similarity	32.0%	Pred No 7.2e-27;		
Matches 74;	Conservative 33;	Mismatches 90;	Indels 34;	Gaps 3;

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QY      29  KPRVQDQSRNHNILQWPGRALTGNSSVYFQYKLMFSCSKSHQKPSGCWQHISCN  88
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Db      39  KRANITFLSINMRNVLQWTPPEGLOGVKVITYTQYFI-----  75

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QY      89  FPGCRITAKYGRQWKNKEDCWGTQELSCDLTSETSDIOEPPYGRVRAASAGSYSEKSMT 148
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Db      76  -----YGGKWLNKSECRNINRTYCDLSAETSDEYHQYAKAKAIWGTGCKSKMAES 126

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QY 149 PRPTPMWETKIDPPVNMITOVNGSLVILHAPNLPYRQKEKNVSIEDYY-ELLYRVFTII 207
DB 127 GREYFLETOIGPEVALITDEKISVYLTAPEKWKRNPEDDLPSMOQIYSNLKYNVSVL 186
QY 208 NNSLEKQKYEGAHRAVEIEALTPHSSCYVAEITYOPMLDRSRSEERC 258
DB 187 NTKSNRTWSQCVTNHTLV-LTWLEPNILYCVHVESFVGPBRRAQPSSEKOC 236

RESULT 8

US-08-943-087-20
; Sequence 20, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-943-087-20

Query Match 21.7%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 7.2e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 29 KPORVQFOSRNFHNILOWOPGRALTGNSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
DB 39 KPAITFTLSIMKNVLTWTPPEGLOGVAVITYVQYFI----- 75
QY 89 FPGGRTIAKYGQROKWKNEKDCWGTQELSDLTSETSDIOEPPYGRVRAASAGSYSEWGMT 148
DB 76 -----YGQKKWLKNSSECRNINRTYCDLSAETSDYEHQYAKKAIWGTCKSKMAES 126
QY 149 PRPTPMWETKIDPPVNMITOVNGSLVILHAPNLPYRQKEKNVSIEDYY-ELLYRVFTII 207
DB 127 GREYFLETOIGPEVALITDEKISVYLTAPEKWKRNPEDDLPSMOQIYSNLKYNVSVL 186

DB 127 GREYFLETOIGPEVALITDEKISVYLTAPEKWKRNPEDDLPSMOQIYSNLKYNVSVL 186
QY 208 NNSLEKQKYEGAHRAVEIEALTPHSSCYVAEITYOPMLDRSRSEERC 258
DB 187 NTKSNRTWSQCVTNHTLV-LTWLEPNILYCVHVESFVGPBRRAQPSSEKOC 236

RESULT 9

US-08-943-087-22
; Sequence 22, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-943-087-22

Query Match 21.7%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 7.2e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 29 KPORVQFOSRNFHNILOWOPGRALTGNSVYFVQYKIMFSCSMKSSHQKPSGCWQHISCN 88
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QY 89 FPGGRTIAKYGQROKWKNEKDCWGTQELSDLTSETSDIOEPPYGRVRAASAGSYSEWGMT 148
DB 76 -----YGQKKWLKNSSECRNINRTYCDLSAETSDYEHQYAKKAIWGTCKSKMAES 126
QY 149 PRPTPMWETKIDPPVNMITOVNGSLVILHAPNLPYRQKEKNVSIEDYY-ELLYRVFTII 207
DB 127 GREYFLETOIGPEVALITDEKISVYLTAPEKWKRNPEDDLPSMOQIYSNLKYNVSVL 186

QY 208 NNSLEKEQKYVGAHRAVEIALTPHSSYCVAEIQLPMLDRSRSEERC 256
| : | : | : | : | : | : | : | : |
Db 187 NTKSNRTWSQCVTNHTLV-LTWLEPNLTLCVHVESFVGPPRRADPSEKOC 236

RESULT 10
US-08-943-087-24
; Sequence 24, Application US/08943087

GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:

Query Match	21.7%	Score 310:	DB 2:	Length 553:
Best Local Similarity	32.0%	Pred. No. 7.2e-27:		
Matches 74: Conservative	33:	Mismatches 90:	Indels 34:	Gaps 3:

Db 187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESEFVPGPPRAQPESEKQC 236

RESULT 11
US-08-943-087-26
; Sequence 26, Application US/08943087
; Patent No. 5945511

APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Fairah, Theresa M.
TITLE OF INVENTION: CITOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:

Query Match	21.7%	Score 310;	DB 2;	Length 553;
Best Local Similarity	32.0%	Pred. No. 7.2e-27;		
Matches 74;	Conservative	33;	Mismatches 90;	Indels 34;
				Gaps 3;

RESULT 12

US-08-943-087-28

; Sequence 28, Application US/08943087

; Patent No. 5945511

; GENERAL INFORMATION:

; APPLICANT: Lok, Si

; APPLICANT: Kho, Choon J.

; APPLICANT: Jelmeberg, Anna C.

; APPLICANT: Adams, Robyn L.

; APPLICANT: Whitmore, Theodore E.

; APPLICANT: Farrah, Theresa M.

; TITLE OF INVENTION: CYTOKINE RECEPTOR

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zymogenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/943,087

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/803,305

; FILING DATE: 20-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Lunn, Paul G

; REGISTRATION NUMBER: 32,743

; REFERENCE/DOCKET NUMBER: 96-24C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6627

; TELEFAX: 206-442-6678

; TELETYPE:

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 553 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-943-087-28

; US-08-943-087-28

; US-08-943-087-28

; US-08-943-087-28

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; US-08-943-087-28

; US-08-943-087-28

US-08-943-087-30

; Sequence 30, Application US/08943087

; Patent No. 5945511

; GENERAL INFORMATION:

; APPLICANT: Lok, Si

; APPLICANT: Kho, Choon J.

; APPLICANT: Jelmeberg, Anna C.

; APPLICANT: Adams, Robyn L.

; APPLICANT: Whitmore, Theodore E.

; APPLICANT: Farrah, Theresa M.

; TITLE OF INVENTION: CYTOKINE RECEPTOR

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zymogenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/943,087

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/803,305

; FILING DATE: 20-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Lunn, Paul G

; REGISTRATION NUMBER: 32,743

; REFERENCE/DOCKET NUMBER: 96-24C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6627

; TELEFAX: 206-442-6678

; TELETYPE:

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 553 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-943-087-30

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; US-08-943-087-30

; US-08-943-087-30

US-08-943-087-32

; Sequence 32, Application US/08943087

; Patent No. 5945511

; GENERAL INFORMATION:

; APPLICANT: Lok, Si

; APPLICANT: Kho, Choon J.

; APPLICANT: Jelmeberg, Anna C.

; APPLICANT: Adams, Robyn L.

; APPLICANT: Whitmore, Theodore E.

; APPLICANT: Farrah, Theresa M.

; TITLE OF INVENTION: CYTOKINE RECEPTOR

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zymogenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/943,087

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/803,305

; FILING DATE: 20-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Lunn, Paul G

; REGISTRATION NUMBER: 32,743

; REFERENCE/DOCKET NUMBER: 96-24C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6627

; TELEFAX: 206-442-6678

; TELETYPE:

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 553 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

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; US-08-943-087-32

; US-08-943-087-32

US-08-943-087-34

; Sequence 34, Application US/08943087

; Patent No. 5945511

; GENERAL INFORMATION:

; APPLICANT: Lok, Si

; APPLICANT: Kho, Choon J.

; APPLICANT: Jelmeberg, Anna C.

; APPLICANT: Adams, Robyn L.

; APPLICANT: Whitmore, Theodore E.

; APPLICANT: Farrah, Theresa M.

; TITLE OF INVENTION: CYTOKINE RECEPTOR

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zymogenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/943,087

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/803,305

; FILING DATE: 20-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Lunn, Paul G

; REGISTRATION NUMBER: 32,743

; REFERENCE/DOCKET NUMBER: 96-24C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6627

; TELEFAX: 206-442-6678

; TELETYPE:

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 553 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-943-087-34

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; US-08-943-087-34

; US-08-943-087-34

US-08-943-087-36

; Sequence 36, Application US/08943087

; Patent No. 5945511

; GENERAL INFORMATION:

; APPLICANT: Lok, Si

; APPLICANT: Kho, Choon J.

; APPLICANT: Jelmeberg, Anna C.

; APPLICANT: Adams, Robyn L.

; APPLICANT: Whitmore, Theodore E.

; APPLICANT: Farrah, Theresa M.

; TITLE OF INVENTION: CYTOKINE RECEPTOR

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zymogenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/943,087

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/803,305

; FILING DATE: 20-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Lunn, Paul G

; REGISTRATION NUMBER: 32,743

; REFERENCE/DOCKET NUMBER: 96-24C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6627

; TELEFAX: 206-442-6678

; TELETYPE:

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

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Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ. ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-32
Query Match 21.7%; Score 310; DB 2; Length 553;
Local Similarity 32.0%; Pred. No. 7,2e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3.
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DB 39 KPAITTELSIMKKKNVLQMTPEGLGVKVTYVYFI----- 75
QY 89 FPGCRTLAKYGORQWKNEDECGTQELSCDLTLETSNDIQEPYGRYRAASAGYSSEMSMT 148
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QY 149 PRETPWMTKTKIDPVMNITQVNGSLVILIAHNPRIYQKEKNVSEIDYY-ELLYVFI 207
DB 127 GRFYFPLETQIGPPEVALTTEDEKSSIVYLADEKWKRNEDLPVSNQQTYSNKTIVSVL 186
QY 208 NNSLEKEQKVEGAHRAVEIAELPHSSVCVAEIIYQPLMDRRSQSEERC 258
DB 187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCIVAVESVTPGPPRAAQSEKQC 236

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APPLICANT: Lok, Si
 APPLICANT: Kho, Choon J.
 APPLICANT: Jelmberg, Anna C.
 APPLICANT: Adams, Robyn L.
 APPLICANT: Whitmore, Theodore E.
 APPLICANT: Farrah, Theresa M.
 TITLE OF INVENTION: CYTOKINE RECEPTOR
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics, Inc.
 STREET: 1201 Eastlake Avenue East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,087
 FILING DATE:
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/803,305
 FILING DATE: 20-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-24C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX:
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 553 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-943-087-34

Search completed: December 22, 2002, 10:15:10
Job time : 28 secs

RESULT 15
US-08-943-087-34
; Sequence 34, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 22, 2002, 10:13:27 : Search time 20 seconds
(without alignments)
219.602 Million cell updates/sec

Title: US-09-964-994-2

Perfect score: 1427

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Number of hits satisfying chosen parameters: 106657

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1213	85.0	231	10	US-09-728-911-2 Sequence 2, Appl 1
2	1213	85.0	231	10	US-09-949-192-6 Sequence 6, Appl 1
3	1104	77.4	210	10	US-09-728-911-13 Sequence 13, Appl 1
4	310	21.7	207	10	US-09-746-359A-65 Sequence 65, Appl 1
5	310	21.7	214	10	US-09-746-359A-63 Sequence 63, Appl 1
6	310	21.7	217	10	US-09-746-359A-55 Sequence 55, Appl 1
7	310	21.7	221	10	US-09-746-359A-12 Sequence 12, Appl 1
8	310	21.7	542	12	US-10-052-586-398 Sequence 54, Appl 1
9	310	21.7	547	10	US-09-746-359A-54 Sequence 54, Appl 1
10	310	21.7	553	10	US-09-746-359A-11 Sequence 11, Appl 1
11	310	21.7	553	10	US-09-949-192-7 Sequence 7, Appl 1
12	310	21.7	559	10	US-09-746-359A-62 Sequence 62, Appl 1
13	310	21.7	571	10	US-09-746-359A-53 Sequence 53, Appl 1
14	310	21.7	594	10	US-09-746-359A-23 Sequence 23, Appl 1
15	289	20.3	56	10	US-09-864-761-40289 Sequence 40289, A
16	289	20.3	56	10	US-09-864-761-40289 Sequence 40289, A
17	276	19.3	217	10	US-09-746-359A-38 Sequence 38, Appl 1
18	276	19.3	514	10	US-09-746-359A-39 Sequence 39, Appl 1
19	276	19.3	546	10	US-09-746-359A-37 Sequence 37, Appl 1

20	240	16.8	574	9	US-09-912-672A-2	Sequence 2, Appl 1
21	240	16.8	574	9	US-10-063-547-164	Sequence 164, App
22	240	16.8	574	10	US-09-728-911-25	Sequence 25, Appl 1
23	240	16.8	574	10	US-09-870-574-4	Sequence 4, Appl 1
24	240	16.8	574	12	US-10-006-867-164	Sequence 164, App
25	237	16.6	574	12	US-09-728-911-34	Sequence 34, Appl 1
26	237	16.6	212	9	US-09-912-672A-6	Sequence 6, Appl 1
27	237	16.6	560	9	US-09-912-672A-5	Sequence 5, Appl 1
28	211	14.8	150	10	US-09-746-359A-66	Sequence 66, Appl 1
29	163	11.4	295	10	US-09-103-067-20	Sequence 20, Appl 1
30	163	11.4	295	10	US-09-949-192-3	Sequence 3, Appl 1
31	159.5	11.2	308	9	US-09-912-672A-23	Sequence 23, Appl 1
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35	152.5	10.7	219	10	US-09-355-000-9	Sequence 9, Appl 1
36	152.5	10.7	578	9	US-09-912-672A-27	Sequence 27, Appl 1
37	152	10.7	211	10	US-09-728-911-36	Sequence 36, Appl 1
38	151.5	10.6	196	10	US-09-746-359A-67	Sequence 67, Appl 1
39	151.5	10.6	201	9	US-09-912-672A-16	Sequence 16, Appl 1
40	151.5	10.6	201	10	US-09-746-359A-59	Sequence 59, Appl 1
41	151.5	10.6	203	10	US-09-746-359A-15	Sequence 15, Appl 1
42	151.5	10.6	282	9	US-09-912-672A-15	Sequence 15, Appl 1
43	151.5	10.6	307	10	US-09-746-359A-58	Sequence 58, App
44	151.5	10.6	311	9	US-09-978-295A-352	Sequence 352, App
45	151.5	10.6	311	9	US-09-992-598-183	Sequence 183, App

ALIGNMENTS

RESULT 1	US-09-728-911-2	Sequence 2, Application US/09728911	
Patent No.	US20020012659A1	GENERAL INFORMATION:	
APPLICANT:	Presnell, Scott R.	APPLICANT:	Xu, Wenfeng
APPLICANT:	Kindsvogel, Wayne	APPLICANT:	Chen, Zhi
TITLE OF INVENTION:	Human Cytokine Receptor	FILE REFERENCE:	99-93
CURRENT APPLICATION NUMBER:	US/09/728,911	CURRENT FILING DATE:	2000-12-01
PRIOR APPLICATION NUMBER:	US 60/169,049	PRIOR FILING DATE:	1999-12-03
PRIOR APPLICATION NUMBER:	US 60/232,219	PRIOR FILING DATE:	2000-09-13
PRIOR APPLICATION NUMBER:	US 60/244,610	NUMBER OF SEQ ID NOS:	36
SOFTWARE:	FastSeq for Windows Version 3.0	SEQ ID NO 2	LENGTH: 231
TYPE:	PRT	ORGANISM:	Homo sapiens
Query Match	85.0%; Score 1213; DB 10; Length 231;	Best Local Similarity	87.8%; Pred. No. 2.4e-109;
Matches 230; Conservative	0; Mismatches 0; Indels 32; Gaps 1;	1	1
1	1	1	1
2	2	2	2
3	3	3	3
4	4	4	4
5	5	5	5
6	6	6	6
7	7	7	7
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31	31	31	31
32	32	32	32
33	33	33	33
34	34	34	34
35	35	35	35
36	36	36	36
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38	38	38	38
39	39	39	39
40	40	40	40
41	41	41	41
42	42	42	42
43	43	43	43
44	44	44	44
45	45	45	45

QY 181 NLPYRQKKNVSIEDYELLVRFITINNSLEKQKVEGAHRAVEIEALTPHSSCYVA 240
DB 150 NLPYRQKKNVSIEDYELLVRFITINNSLEKQKVEGAHRAVEIEALTPHSSCYVA 209
QY 241 EIIQPMIDRRSQRSEKCEVEIP 262
DB 210 EIIQPMIDRRSQRSEKCEVEIP 231

RESULT 2
US-09-949-192-6
Sequence 6, Application US/094949192
Patent No. US20020142292A1

GENERAL INFORMATION:
APPLICANT: Parham, Christi L.
APPLICANT: Gorman, Daniel L.
APPLICANT: Kurata, Hirokazu
APPLICANT: Arai, Naoko
APPLICANT: Sana, Theodore R.
APPLICANT: Mattson, Jeanine D.
APPLICANT: Murphy, Erin E.
APPLICANT: Savkoor, Chetan
APPLICANT: Grein, Jeffery
APPLICANT: Smith, Kathleen M.
APPLICANT: McClanahan, Terrill K.
TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX01169K
CURRENT APPLICATION NUMBER: US/09/949,192
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/231,267
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 231
TYPE: PRT
ORGANISM: Homo sapiens
US-09-949-192-6

Query Match 85.0%; Score 1213; DB 10; Length 231;
Best Local Similarity 87.8%; Pred. No. 2,4e-109;
Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPRHCFGLISFLTGVAGOSTHESLKPORVOFOSRNFHNILOMOPGRALTGSSVYF 60
DB 2 MPRHCFGLISFLTGVAGOSTHESLKPORVOFOSRNFHNILOMOPGRALTGSSVYF 61
DB 61 VOYKIMFSCSMKSSHOKRPGSCWQHISCNFPCRTLAKYQORQKNEKDCWGTQELSCDUT 120
DB 62 VOYKI-----YGOQWKNKEDCWGTQELSCDUT 89
QY 121 SETSDIOEPYGRVRAASAGSYSMSMTPRTPWMTKIDPPVANNITOVNGSLVILHAP 180
DB 90 SETSDIOEPYGRVRAASAGSYSMSMTPRTPWMTKIDPPVANNITOVNGSLVILHAP 149
QY 181 NLPYRQKKNVSIEDYELLVRFITINNSLEKQKVEGAHRAVEIEALTPHSSCYVA 240
DB 150 NLPYRQKKNVSIEDYELLVRFITINNSLEKQKVEGAHRAVEIEALTPHSSCYVA 209
QY 241 EIIQPMIDRRSQRSEKCEVEIP 262
DB 210 EIIQPMIDRRSQRSEKCEVEIP 231

RESULT 3
US-09-728-911-13
Sequence 13, Application US/09728911
Patent No. US20020012669A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Xu, Wenteng
APPLICANT: Kindsvogel, Wayne

APPLICANT: Chen, Zhi
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 99-93
CURRENT APPLICATION NUMBER: US/09/728,911
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 60/169,049
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US 60/232,219
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: US 60/244,610
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 210
TYPE: PRT
ORGANISM: Homo sapiens
US-09-728-911-13

Query Match 77.4%; Score 1104; DB 10; Length 210;
Best Local Similarity 86.8%; Pred. No. 6,3e-99;
Matches 210; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 21 TQSTHESLKPORVOFOSRNFHNILOMOPGRALTGSSVYFVOYKIMFSCSMKSSHOKRPG 80
DB 1 TQSTHESLKPORVOFOSRNFHNILOMOPGRALTGSSVYFVOYKI----- 45
QY 81 CWOHISCNFPCRTLAKYQORQKNEKDCWGTQELSCDUTSETSDIOEPYGRVRAASAG 140
DB 46 -----YGOQWKNKEDCWGTQELSCDUTSETSDIOEPYGRVRAASAG 88
QY 141 SYSMSMTPRTPWMTKIDPPVANNITOVNGSLVILHAPNLPYRQKKNVSIEDYEL 200
DB 89 SYSMSMTPRTPWMTKIDPPVANNITOVNGSLVILHAPNLPYRQKKNVSIEDYEL 148
QY 201 LVYRFTINNSLEKQKVEGAHRAVEIEALTPHSSCYVAEIIQPMIDRRSQRSEKCE 260
DB 149 LVYRFTINNSLEKQKVEGAHRAVEIEALTPHSSCYVAEIIQPMIDRRSQRSEKCE 208
QY 261 IP 262
DB 209 IP 210

RESULT 4
US-09-746-359A-65
Sequence 65, Application US/09746359A
Patent No. US20020042366A1
GENERAL INFORMATION:
APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenteng
APPLICANT: Madden, Karen L.
APPLICANT: Kelly, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
APPLICANT: Eagan, Maribeth A.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekhar, Yashin A.
APPLICANT: No. US20020042366A1ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 65
LENGTH: 207
TYPE: PRT

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ORGANISM: Homo sapiens
US-09-746-359A-65

Query Match
Best Local Similarity 32.0%; Score 310; DB 10; Length 207;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 29 KPGVQFOSRNFHNILOMPGRALTGNSVYFVQYKIMFSCMSKSSHQKPSGCMQHISCN 88
DB 3 KPANITFLSINMKNVLOMTPEGLQGVKVTYVQYFI----- 39
QY 89 FPGCRTLAKYQORQKNEKDCWGTQELSCDITSETSDIQEPYGRVRAASAGSYSEMSMT 148
DB 40 -----YGOKKWLKSECRNINRTYCDLSAETSDYEHQYAKKAIWGTCKSKMAES 90
QY 149 PRTPWMTETKIDPPVNNITQVNGSLVILHAPNLPYRQKEKNVSIEDY-ELLYRVFII 207
DB 91 GRFPFLETOIGPEVALITDEKSIYVLTAPKWKRNPEDLPVSMQOITYSNLKYNSVL 150
QY 208 NNSLEKEQKVEGAHRAVEIALTPHSSYCVAAEIIYOPMLDRSQRSEERC 258
DB 151 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVGPPRRAPQSEKQC 200

RESULT 5
US-09-746-359A-63
Sequence 63, Application US/09746359A
Patent No. US20020042366A1
GENERAL INFORMATION:
APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenteng
APPLICANT: Madden, Karen L.
APPLICANT: Kelly, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
APPLICANT: Eagan, Maribeth A.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekher, Yashin A.
APPLICANT: No. US20020042366A1ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 63
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
US-09-746-359A-63

Query Match
Best Local Similarity 21.7%; Score 310; DB 10; Length 214;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 29 KPGVQFOSRNFHNILOMPGRALTGNSVYFVQYKIMFSCMSKSSHQKPSGCMQHISCN 88
DB 10 KPANITFLSINMKNVLOMTPEGLQGVKVTYVQYFI----- 46
QY 89 FPGCRTLAKYQORQKNEKDCWGTQELSCDITSETSDIQEPYGRVRAASAGSYSEMSMT 148
DB 47 -----YGOKKWLKSECRNINRTYCDLSAETSDYEHQYAKKAIWGTCKSKMAES 97
QY 149 PRTPWMTETKIDPPVNNITQVNGSLVILHAPNLPYRQKEKNVSIEDY-ELLYRVFII 207
DB 98 GRFPFLETOIGPEVALITDEKSIYVLTAPKWKRNPEDLPVSMQOITYSNLKYNSVL 157
QY 208 NNSLEKEQKVEGAHRAVEIALTPHSSYCVAAEIIYOPMLDRSQRSEERC 258
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DB 158 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVGPPRRAPQSEKQC 207

RESULT 6
US-09-746-359A-55
Sequence 55, Application US/09746359A
Patent No. US20020042366A1
GENERAL INFORMATION:
APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenteng
APPLICANT: Madden, Karen L.
APPLICANT: Kelly, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
APPLICANT: Eagan, Maribeth A.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekher, Yashin A.
APPLICANT: No. US20020042366A1ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 55
LENGTH: 217
TYPE: PRT
ORGANISM: Homo sapiens
US-09-746-359A-55

Query Match
Best Local Similarity 21.7%; Score 310; DB 10; Length 217;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 29 KPGVQFOSRNFHNILOMPGRALTGNSVYFVQYKIMFSCMSKSSHQKPSGCMQHISCN 88
DB 10 KPANITFLSINMKNVLOMTPEGLQGVKVTYVQYFI----- 46
QY 89 FPGCRTLAKYQORQKNEKDCWGTQELSCDITSETSDIQEPYGRVRAASAGSYSEMSMT 148
DB 47 -----YGOKKWLKSECRNINRTYCDLSAETSDYEHQYAKKAIWGTCKSKMAES 97
QY 149 PRTPWMTETKIDPPVNNITQVNGSLVILHAPNLPYRQKEKNVSIEDY-ELLYRVFII 207
DB 98 GRFPFLETOIGPEVALITDEKSIYVLTAPKWKRNPEDLPVSMQOITYSNLKYNSVL 157
QY 208 NNSLEKEQKVEGAHRAVEIALTPHSSYCVAAEIIYOPMLDRSQRSEERC 258
DB 158 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVGPPRRAPQSEKQC 207

RESULT 7
US-09-746-359A-12
Sequence 12, Application US/09746359A
Patent No. US20020042366A1
GENERAL INFORMATION:
APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenteng
APPLICANT: Madden, Karen L.
APPLICANT: Kelly, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
APPLICANT: Eagan, Maribeth A.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekher, Yashin A.
APPLICANT: No. US20020042366A1ak, Julia E.
```

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; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 12
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-746-359A-12

Query Match      21.7%; Score 310; DB 10; Length 221;
Best Local Similarity 32.0%; Pred. No. 1,4e-22;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

29 KPRVQFOSNFHIILOWOGRAITGSSVYFYQYKIMFSCSMKSSHQKPSGCMHISCN 88
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
10 KPANITFLSINMKVGLWTPREGIQLGVKVTYTYFYFI----- 46
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
89 FPCRTLAKYGOROMKKECDMGTOELSCDLTSETSDIOEPYGRVRAASAGSYSEWMT 148
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
47 -----YQKKMLNKSECRNINRTYCDLSAETSDHEQYKAKIWMGKCKMAES 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
149 PRFTPMWETKIDPVMNITGVNSSLVILHAPNLPYRQKKNVSIEDYY-ELLYRVFII 207
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
98 GRYPFLETOIGPREVALTDEKISIVLTAPKWKRNDELPVSMQOISMLKYNVSVL 157
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
208 NNSLEKQKYEAGHRAVETALPHSSCYVALETYOMDMRDSRSEERC 258
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
158 NTKSNRTWSOCVTNHTLV-LTWLEPNTLYCVHSEFVGPERRAOPSEKOC 207
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
; Sequence 398, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
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;; PRIOR APPLICATION NUMBER: 60/083559
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086023
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/086392
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/086486
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087098
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087208
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
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;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
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;; PRIOR APPLICATION NUMBER: 60/088811
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088825
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088861

;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088863
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089090
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089908

Query Match 21.7%; Score 310; DB 12; Length 542;
Best Local Similarity 32.0%; Pred. No. 4.6e-22;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 29 KPGKVOGOSRNFHNIIOWQGRALTGSSVYFOYKIMFSCSMKSHQKPSGCMQHISCN 88
DB 28 KPNITFLSTNKNVLOMPPEGLQGVKVTYVOYFT----- 64
QY 89 FPGCRITLANYGQROKRNKEDCMGTQELSCDLTSETSDIOPEYGRVRAASGSYSEMSMT 148
DB 65 -----YGOCKKWLNSKSCRNINRTYCDLSAFTSDYEHQYAKVAINGTKSKNAES 115
QY 149 PRTPWETKIDPPVANNITOVNGLVILHAPMLPYRQKEKNVSIEDYV-ELLYRVFTI 207
DB 116 GREYPLETQIGPPEVALTTDEKSIISVLTAPPEKRNRPEDLPVSMQOIVSNLKYNSVL 175
QY 208 NNSLEKEQKYEGAHRAVEATEALPHSSYCVVAEIYQPMIDRRSQREENC 258
DB 176 NTKSNTWSQCVNHTLV-LTWLEPNILCVHVESFVGPGRRAQPSKOC 225

RESULT 9
US-09-746-359A-54
; Sequence 54, Application US/09746359A
; Patent No US20020042366A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yashin A.
; APPLICANT: No US20020042366A1ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; PRIOR APPLICATION NUMBER: 2001-05-21
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 547
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-746-359A-54


```

? TITLE OF INVENTION: Method for Treating Inflammation
?
? FILE REFERENCE: 99-108
?
? CURRENT APPLICATION NUMBER: US/09/746,359A
?
? CURRENT FILING DATE: 2001-05-21
?
? PRIOR APPLICATION NUMBER: 60/171,969
?
? PRIOR FILING DATE: 1999-12-23
?
? PRIOR APPLICATION NUMBER: 60/213,341
?
? PRIOR FILING DATE: 2000-06-22
?
? NUMBER OF SEQ ID NOS: 72
?
? SOFTWARE: FastSeq for Windows Version 3.0
?
? SEQ ID NO 62
?
? LENGTH: 559
?
? TYPE: PRT
?
? ORGANISM: Homo sapiens
?
US-09-746-359A-62

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	Query Match	21.7%	Score 310;	DB 10;	Length 559;
	Best Local Similarity	32.0%;	Pred. No. 4.7e-22;		
	Matches	74;	Conservative	33;	Mismatches 90; Indels 34; Gaps 3
Db	29	KPQVQFQSRNFHNILOWPGFALGTGNSVYFYQYKIMFSCMSKSHOKPSCGWOHISCN	88		
	10	KPANIITLSTIMMKVNLWLOFPREGLOGVYTYVQYFI-----	46		
QY	89	FPQGRTLAKYGOBOMKNEKDCWGTQELSCDLTSEFSDIOEPYGGVRAASAGSYSEMSMT	148		
Db	47	-----YGQKKMLKSECRNINRTYCDLSAETSDYDEHQYAKVKAIMGTCKSGMAES	97		
QY	149	PRTPFWETKIDPPVMMNITVOYNSGLVILHAPNLPYRQKEKNVSIEDY-ELLYRVFI	207		
Db	98	GRFPELETFQIGPREVALTTDEKISVLTLPDEKMRNPEDLPVMOQIYSULKYNVSL	157		
QY	208	NNSLKEOKYEGAHRAVEIETALPPHSYCVVAETIYOMLDRSQRSERC	258		
Db	158	NTKSNRTWCQVTHNLLV-LTWLEPNTLYCYHVSFVDPGPRRKPDSKOC	207		

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US-09-746-359A-53
RESULT 13
US-09-746-359A-53
Sequence 53, Application US/09746359A
Patent No. US20020042366A1
GENERAL INFORMATION:
APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenfeng
APPLICANT: Madden, Karen L.
APPLICANT: Kelly, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Blumberg, Hal
APPLICANT: Eagan, Maribeth A.
APPLICANT: Jaspers, Stephen R.
APPLICANT: Chandrasekher, Yashmin A.
APPLICANT: No. US20020042366A1ax, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 53
LENGTH: 571
TYPE: PRT
ORGANISM: Homo sapiens
US-09-746-359A-53

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Query Match	21.7%	Score 310;	DB 10;	Length 571;
Best Local Similarity	32.0%	Pred. NO. 4.9e-22;		
Matches	74; conservative	33; mismatches	90; indels	34; gaps

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0Y      KPQRFQFSRNFHNTLQMOQPGHALTNGNSVYFYQKMFSCSMSSHOKBEGCQMOHISCN  88
Db      KPANITFELSINKKNVLOWTTPBEGLOGVAYTVYQFY-----  70
0Y      PFGCFTLAKYGOROKNKNEDCWTGOTELSCDLTTFESDSIOEYGRVRAASAGSYSENSMT  146
Db      -----YQCKWLKNSSECRNINRYICDLSAELSDYEHQYKAKYAKIMTKCKSKMAES  122
0Y      PRFTFWMETKIDPRPMNITQVNGSLVTLHAPNLPRYQKEKNYSIEDY-ELLYRYFII  207
Db      122 GRFPELETQIGPREVALATTEDEKSSISVULTAPEKMRNPEDLPYMQOIIYSLKAYNSVL  182
0Y      NNSLEKEQYVEGAHRAVEIEALPRHSSCYVAELIYQPMIDRQRQREBERC  258
Db      182 NTKSRMTSQCVTNHTLY-LTWLEPNLILCHVNESFVGPGRPRRQAPSEKQ  231

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RESULT 14
US-09-746-359A-23
; Sequence 23, Application US/09746359A
; Patent No. US20020042366A1
GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-23

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	Query Match	21.7%	Score 310:	DB 10:	Length 594:
	Best Local Similarity	32.0%:	Pred. No. 5,1e-22:		
	Matches	74:	Conservative	33:	Mismatches 90: Indels 34: Gaps 3:
QY	29	KPQRVDFQSNNFHNIILQWOPGRALITGSSVYEVOYKIMFSCSMKSSHOKPSGCWOHISGN	88		
		: : : : : :			
Db	45	KPANIIFLLINMKNVLTOWTEPEEGLOGKVITYGYFI-----	81		
QY	89	FPCRIPLAKYGROMKKEQCMWGFOELSCDILTSTSDIQEPIYGRVRAASGSYSMSMT	148		
		: : : : : : : : : :			
Db	82	-----YGCKKIWLKSECRNINRYICDLASLTSDEHOHYAVKVKIWTCTSKMAES	132		
QY	149	PRTPPWETKIDPPVMNITGVNSGLVILHAPNLPYRQKEKNYSIEDY-ELIYRVFLI	207		
		: : : : : : : : : : : : :			
Db	133	GREYFELETDIGCPREALTDEKSISVLNAPEKWKRNRPEDLPVSMQOIIYNLKYNVSL	192		
QY	208	NNSLREKQKYEGSAHRVELTEALLPHSYCYVAETIYPMIDRSQRSEERC	258		
		: : : : : : : : : : : : : : :			
Db	193	NKSNRTWSOCVTNNHLV-LTWLEPNLVLCVHNESFVGCPRRARQSPKQC	242		

RESULT 15
US-09-864-761-40289
; Sequence 40289, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

NO ID NO 40289

LENGTH: 56

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: MAP TO AL158138.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3

OTHER INFORMATION: SWISSPROT HIT: O28438, EVALUATE 1.20e+00

OTHER INFORMATION: EST_HUMAN HIT: AV14177.1, EVALUATE 4.00e-26

US-09-864-761-40289

Query Match 20.3%; Score 289; DB 10; Length 56;

Best Local Similarity 100.0%; Pred. No. 2.4e-21;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 KIDPPVNNITQVNGSLVLIHAPNLPYRYQEKKNVSIEDYYELLYRVFIINNSLEK 213

|||||

DB 1 KIDPPVNNITQVNGSLVLIHAPNLPYRYQEKKNVSIEDYYELLYRVFIINNSLEK 56

Search completed: December 22, 2002, 10:21:48
Job time: 22 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 22, 2002, 10:06:17 ; Search time 80 Seconds
(without alignments)
674.804 Million cell updates/sec

Title: US-09-964-994-2
Perfect score: 1427
Sequence: 1 MPNHCEGLISFLGAGVAG.....YQPMIDRRSRQSEKVEIP 262

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1427	100.0	263	4 Q969J5	Q969J5 homo sapien
2	1213	85.0	231	4 Q96A41	Q96A41 homo sapien
3	664	46.5	130	4 Q96OR0	Q96OR0 homo sapien
4	310	21.7	553	4 Q96H4	Q96H4 homo sapien
5	310	21.7	553	4 Q96SH8	Q96SH8 homo sapien
6	262	18.4	209	4 Q96SH7	Q96SH7 homo sapien
7	240	16.8	574	4 Q96H22	Q96H22 homo sapien
8	187.5	13.1	569	4 Q96ND6	Q96ND6 ratu mus norv
9	180.5	12.6	341	13 Q96G8	Q96G8 gallu gall
10	173.5	12.2	294	13 Q96OM13	Q96OM13 oncorhynch
11	155.5	10.9	569	13 Q96YH0	Q96YH0 gallu gall
12	152.5	10.7	442	13 Q96YJ9	Q96YJ9 gallu gall
13	149.5	10.5	325	4 Q96BU4	Q96BU4 homo sapien
14	149	10.4	351	11 Q8VHM7	Q8VHM7 mus musculu
15	136.5	9.6	557	4 Q8WT22	Q8WT22 mus musculu
16	126	8.8	294	11 Q8R3Q1	Q8R3Q1 mus musculu

17	121.5	8.5	508	13 Q9YHV9	Q9YHV9 gallu gall
18	119.5	8.4	508	13 Q9PYK0	Q9PYK0 gallu gall
19	118.5	8.3	489	4 Q9BT69	Q9BT69 homo sapien
20	115.5	8.1	332	6 Q9GK86	Q9GK86 ovis aries
21	110.5	7.7	332	11 Q63953	Q63953 mus musculu
22	108	7.6	484	4 Q14936	Q14936 homo sapien
23	101.5	7.1	239	4 Q15467	Q15467 homo sapien
24	101.5	7.1	331	4 Q9BUD0	Q9BUD0 homo sapien
25	100.5	7.0	608	6 Q9N077	Q9N077 monodelphis
26	95	6.7	1253	12 Q9JGK8	Q9JGK8 sagiyama vi
27	93	6.5	453	16 Q9K434	Q9K434 streptomyc
28	92.5	6.4	1155	17 Q8TP28	Q8TP28 methanosarc
29	91.5	6.4	424	11 Q91YA2	Q91YA2 mus musculu
30	88	6.2	745	10 Q9ALO3	Q9ALO3 oryza sativ
31	88	6.2	795	11 Q9CRF5	Q9CRF5 mus musculu
32	88	6.2	2320	5 Q9XTM9	Q9XTM9 trichomonas
33	87.5	6.1	674	13 Q90369	Q90369 coturnix co
34	87.5	6.1	675	13 Q9PSH7	Q9PSH7 gallu gall
35	87.5	6.1	2959	11 Q9JIF1	Q9JIF1 ratu mus norv
36	87	6.1	304	4 Q9Y504	Q9Y504 homo sapien
37	87	6.1	1145	12 Q87049	Q87049 semliki for
38	87	6.1	1244	12 Q88628	Q88628 chikungunya
39	87	6.1	1384	4 Q75257	Q75257 homo sapien
40	86.5	6.1	392	11 Q99KP5	Q99KP5 mus musculu
41	86.5	6.1	632	6 Q95ML5	Q95ML5 salmifri bol
42	86.5	6.1	1083	5 Q9W071	Q9W071 dtosophila
43	86.5	6.1	1289	4 Q9Y2A5	Q9Y2A5 homo sapien
44	86	6.0	477	11 Q91Y85	Q91Y85 mus musculu
45	85.5	6.0	1002	15 Q91M29	Q91M29 human immun

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	263 AA.
Q969J5	01-DEC-2001 (TREMBLrel. 19, Created)		
Q969J5	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
Q969J5	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
Q969J5	Soluble cytokine class II receptor, long isoform precursor (Interleukin 22-binding protein CRP2-10L).		
Q969J5	CRF2-S1 OR IL22BP.		
Q969J5	Homo sapiens (Human).		
Q969J5	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
Q969J5	NCBI_TaxID=9606;		
Q969J5	[1]		
Q969J5	SEQUENCE FROM N.A.		
Q969J5	TISSUE=PLACENTA;		
Q969J5	MEDLINE=21518574; PubMed=11607789;		
Q969J5	Wolk K., Asadullah K., Sabat R.;		
Q969J5	"A novel, soluble homologue of the human IL-10 receptor with preferential expression in Placenta.";		
Q969J5	Genes Immun. 2:329-334(2001).		
Q969J5	[2]		
Q969J5	SEQUENCE FROM N.A.		
Q969J5	MEDLINE=21286453; PubMed=11390454;		
Q969J5	Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,		
Q969J5	Dikensheets H., Donnelly R.P., Pestka S.;		
Q969J5	"Identification, cloning, and characterization of a novel soluble receptor that binds IL-22 and neutralizes its activity.";		
Q969J5	J. Immunol. 166:7096-7103(2001).		
Q969J5	EMBL: AJ313162; CAC85635.1;		
Q969J5	EMBL: AY040567; AAK85715.1;		
Q969J5	InterPro: IPR000282; Cytok_receptor_2.		
Q969J5	Receptor; signal.		
Q969J5	SIGNAL	1	21
Q969J5	CHAIN	22	263
Q969J5	POTENTIAL.		
Q969J5	SOLUBLE CYTOKINE CLASS II RECEPTOR, LONG ISOFORM.		
Q969J5	SEQUENCE	263 AA;	30550 MW; C96EC5D7BAC79B CRC64;

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Query Match      100.0%; Score 1427; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.4e-129;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPKHCFGLISFELTAVAGTOSTHESLKPORVOFOSRNFHNILOMPGRALTGNSSYF 60
   |||||||
DB 2 MPKHCFGLISFELTAVAGTOSTHESLKPORVOFOSRNFHNILOMPGRALTGNSSYF 61

QY 61 VOXKIMFSCMSKSHOKPSGCWQHISCNFPGCRTLAKYGGOROMKNEKDCWGTQELSCDLT 120
   |||||||
DB 62 VOXKIMFSCMSKSHOKPSGCWQHISCNFPGCRTLAKYGGOROMKNEKDCWGTQELSCDLT 121

QY 121 SETSDIOEPYGGVRAASAGSYSEMSMTPTPTPWETKIDPPVNNITQVNGSLIYLHAP 180
   |||||||
DB 122 SETSDIOEPYGGVRAASAGSYSEMSMTPTPTPWETKIDPPVNNITQVNGSLIYLHAP 181

QY 181 NLPYRQKEKNVSIEDYELLRYVFIIINNSLEKQKYEGAHRAVEIALTPHSSYCYVA 240
   |||||||
DB 182 NLPYRQKEKNVSIEDYELLRYVFIIINNSLEKQKYEGAHRAVEIALTPHSSYCYVA 241

QY 241 EIQPMLDRRSORSERCVEIP 262
   |||||||
DB 242 EIQPMLDRRSORSERCVEIP 263

RESULT 2
096A41 PRELIMINARY; PRT; 231 AA.
ID 096A41;
AC 096A41;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Soluble cytokine class II receptor, short isoform precursor
DE (interleukin 22-binding protein CRF2-10) (class II cytokine receptor)
DE (interleukin 22 binding protein).
DE CRF2-1 OR IL22BP OR IL22RA2 OR IL-22BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA MEDLINE-21518574; PubMed=11607789;
RA Gruenberg B.H., Schoenmeyer A., Weiss B., Toschi L., Kunz S.,
RA Wolk K., Asaduliah K., Sabat R.,
RA "A novel, soluble homologue of the human IL-10 receptor with
RA preferential expression in placenta.";
RA Genes Immun. 2:329-334(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE-21286453; PubMed=11390454;
RA Kolenko S.V., Izotova L.S., Mitrochitchenko O.V., Esterova E.,
RA Dickensheets H., Donnelly R.P., Pestka S.;
RA "Identification, cloning, and characterization of a novel soluble
RA receptor that binds IL-22 and neutralizes its activity.";
RA J. Immunol. 166:7096-7103(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE-21396522; PubMed=11491447;
RA Xu W., Presnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,
RA Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeyer S.,
RA Yeo L., Whitmore T.E., Chandrasekhar Y., Grant F.J., Maurer M.,
RA Jelinek L., Storey D.C., Brender T., Hammond A., Topouzis S.,
RA Clegg C.H., Foster H.,
RA "A soluble class II cytokine receptor, IL-22RA2, is a naturally
RA occurring IL-22 antagonist.";
RA Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=BRST;
RA Dumoutier L., Lejeune D., Renaud J.C.;

```

```

RT "Cloning and characterization of Interleukin-22 Binding Protein (IL-
RT 22BP), a natural antagonist of IL-TIF/IL-22.";
RL Submitted (DEC-2000) to the EMBL/Genbank/DBD databases.
DR EMBL, AJ313161; CAC85634.1; -
DR EMBL, AY040566; AAK85714.1; -
DR EMBL, AY044429; AAK91775.1; -
DR EMBL, AJ297262; CAC83097.1; -
DR InterPro: IPR000282; Cytok_receptor_2.
KM Receptor; Signal.
FT SIGNAL 1 21
FT CHAIN 22 231
FT ISOFORM.
SQ SEQUENCE 231 AA; 26979 MW; 2A6912BFF75100F CRC64;

Query Match      85.0%; Score 1213; DB 4; Length 231;
Best Local Similarity 87.8%; Pred. No. 8.3e-109;
Matches 230; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPKHCFGLISFELTAVAGTOSTHESLKPORVOFOSRNFHNILOMPGRALTGNSSYF 60
   |||||||
DB 2 MPKHCFGLISFELTAVAGTOSTHESLKPORVOFOSRNFHNILOMPGRALTGNSSYF 61

QY 61 VOXKIMFSCMSKSHOKPSGCWQHISCNFPGCRTLAKYGGOROMKNEKDCWGTQELSCDLT 120
   |||||||
DB 62 VOXKI-----YGGOROMKNEKDCWGTQELSCDLT 89

QY 121 SETSDIOEPYGGVRAASAGSYSEMSMTPTPTPWETKIDPPVNNITQVNGSLIYLHAP 180
   |||||||
DB 90 SETSDIOEPYGGVRAASAGSYSEMSMTPTPTPWETKIDPPVNNITQVNGSLIYLHAP 149

QY 181 NLPYRQKEKNVSIEDYELLRYVFIIINNSLEKQKYEGAHRAVEIALTPHSSYCYVA 240
   |||||||
DB 150 NLPYRQKEKNVSIEDYELLRYVFIIINNSLEKQKYEGAHRAVEIALTPHSSYCYVA 209

QY 241 EIQPMLDRRSORSERCVEIP 262
   |||||||
DB 210 EIQPMLDRRSORSERCVEIP 231

RESULT 3
096OR0 PRELIMINARY; PRT; 130 AA.
ID 096OR0;
AC 096OR0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Interleukin 22-binding protein CRF2-10S.
DE IL22BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-21286453; PubMed=11390454;
RA Kolenko S.V., Izotova L.S., Mitrochitchenko O.V., Esterova E.,
RA Dickensheets H., Donnelly R.P., Pestka S.;
RA "Identification, cloning, and characterization of a novel soluble
RA receptor that binds IL-22 and neutralizes its activity.";
RA J. Immunol. 166:7096-7103(2001).
DR EMBL, AY040568; AAK85716.1; -
DR InterPro: IPR000282; Cytok_receptor_2.
SQ SEQUENCE 130 AA; 15128 MW; A165814C641F5E5B CRC64;

Query Match      46.5%; Score 664; DB 4; Length 130;
Best Local Similarity 79.5%; Pred. No. 3.2e-56;
Matches 124; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPKHCFGLISFELTAVAGTOSTHESLKPORVOFOSRNFHNILOMPGRALTGNSSYF 60
   |||||||
DB 2 MPKHCFGLISFELTAVAGTOSTHESLKPORVOFOSRNFHNILOMPGRALTGNSSYF 61

QY 61 VOXKIMFSCMSKSHOKPSGCWQHISCNFPGCRTLAKYGGOROMKNEKDCWGTQELSCDLT 120

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Db 62 VQKTI-----YQGRQWKNKEDCGTQELSCDLT 89
QY 121 SETSDIOEPYGRVRAASAGSYSEMSMTPRTTPWME 156
Db 90 SETSDIOEPYGRVRAASAGSYSEMSMTPRTTPWME 125

RESULT 4
Q90HF4 PRELIMINARY; PRT; 553 AA.
AC Q90HF4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Class II cytokine receptor ZCYTOR7.
GN ZCYTOR7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP Lok S., Kho C., Jeimberg A., Adams R., Whitmore T., Farrah T.,
RA O'Hara P.;
RT "Homo sapiens cytokine receptor homolog.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RP Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehnert J.,
RA Martinez T., Hoffman R., O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF184971; AAF01320.1; -.
DR HSSP: P13726; 2HFT.
DR InterPro: IPR000282; Cytok_receptor_2.
DR InterPro: IPR001187; Tissue_factor.
DR Pfam: PF01108; Tissue_fac; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 553 AA; 62533 MW; 7C23C8543B114659 CRC64;

Query Match 21.7%; Score 310; DB 4; Length 553;
Best Local Similarity 32.0%; Pred. No. 2.2e-21;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 29 KQRVQFOSRNFHNILOMPGRALTGNSSVFYQYKIMFSCSMKSSHOKPSGCMQHISCN 88
Db 39 KPNATITFLSINKMKNVLOMPPEGLOGVKVYTYVQYFI----- 75
89 FPGCRTLAKYQGRQWKNKEDCGTQELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMT 148
76 -----YQGRQWKNKEDCGTQELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMT 126
149 PRTPPWMEETKIDPPVNNITQVNGSLVILHAPNLPYRYQKEKNVSIEDY-ELLYRVFII 207
Db 127 GRYPPLFLEIQIGPEVALTIDKESISVLTAPBEKMKRNPEDLPVSMQOYISNLKYNVSVL 186
208 NNSLEKEQKYEGAGRAVEIEALTPHSSYCVVAEITYQPMIDRFSQSRSEEC 258
187 NTKSNRTWQSCVNTNHTLV-LTWLEPNILYCVHVESFVPGPPRRAPSEKOC 236

RESULT 5
Q96SH8 PRELIMINARY; PRT; 553 AA.
AC Q96SH8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BA204P2.1.1 (interleukin 20 receptor alpha, isoform 1).
GN IL20RA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Griffiths C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL135902; CAC38375.1; -.
DR InterPro: IPR000282; Cytok_receptor_2.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR001187; Tissue_factor.
DR Pfam: PF01108; Tissue_fac; 1.
DR SMART: SM00060; FN3; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 553 AA; 62485 MW; D5C2621FDC848328 CRC64;

Query Match 21.7%; Score 310; DB 4; Length 553;
Best Local Similarity 32.0%; Pred. No. 2.2e-21;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 29 KQRVQFOSRNFHNILOMPGRALTGNSSVFYQYKIMFSCSMKSSHOKPSGCMQHISCN 88
Db 39 KPNATITFLSINKMKNVLOMPPEGLOGVKVYTYVQYFI----- 75
89 FPGCRTLAKYQGRQWKNKEDCGTQELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMT 148
76 -----YQGRQWKNKEDCGTQELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMT 126
149 PRTPPWMEETKIDPPVNNITQVNGSLVILHAPNLPYRYQKEKNVSIEDY-ELLYRVFII 207
Db 127 GRYPPLFLEIQIGPEVALTIDKESISVLTAPBEKMKRNPEDLPVSMQOYISNLKYNVSVL 186
208 NNSLEKEQKYEGAGRAVEIEALTPHSSYCVVAEITYQPMIDRFSQSRSEEC 258
187 NTKSNRTWQSCVNTNHTLV-LTWLEPNILYCVHVESFVPGPPRRAPSEKOC 236

RESULT 6
Q96SH7 PRELIMINARY; PRT; 209 AA.
AC Q96SH7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE BA204P2.1.3 (interleukin 20 receptor alpha, isoform 3).
GN IL20RA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP Griffiths C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL135902; CAC38376.1; -.
DR InterPro: IPR000282; Cytok_receptor_2.
DR InterPro: IPR000282; Cytok_receptor_2.
KW Receptor.
SQ SEQUENCE 209 AA; 23616 MW; 467AB77BE3840361 CRC64;

Query Match 18.4%; Score 262; DB 4; Length 209;
Best Local Similarity 31.1%; Pred. No. 2.9e-17;
Matches 61; Conservative 29; Mismatches 72; Indels 34; Gaps 3;

QY 29 KQRVQFOSRNFHNILOMPGRALTGNSSVFYQYKIMFSCSMKSSHOKPSGCMQHISCN 88
Db 39 KPNATITFLSINKMKNVLOMPPEGLOGVKVYTYVQYFI----- 75
89 FPGCRTLAKYQGRQWKNKEDCGTQELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMT 148
76 -----YQGRQWKNKEDCGTQELSCDLTSETSDIOEPYGRVRAASAGSYSEMSMT 126
149 PRTPPWMEETKIDPPVNNITQVNGSLVILHAPNLPYRYQKEKNVSIEDY-ELLYRVFII 207
Db 127 GRYPPLFLEIQIGPEVALTIDKESISVLTAPBEKMKRNPEDLPVSMQOYISNLKYNVSVL 186
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QY 208 NNSLEKQKV-YEGAH 222
| : : : :
DB 187 NTKSNRTVSLKMGAV 202

RESULT 7
Q9HB22 PRELIMINARY; PRT; 574 AA.
AC Q9HB22;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE IL-22 receptor.
GN IL22R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN (1)
SEQUENCE FROM N.A.
MEDLINE=20469498; PubMed=10875937;
Xie M.H., Aggarwal S., Ho W.H., Foster J., Zhang Z., Stinson J.,
Wood W.I., Goddard A.D., Gurney A.L.;
"Interleukin (IL)-22, a Novel Human Cytokine That Signals through the
Interferon Receptor-Related Proteins CRF2-4 and IL-22R.";
RL J. Biol. Chem. 275:31335-31339(2000).
DR EMBL; AF286095; AAG22073.1; -.
DR HSSP; P13726; 1TFH.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor.
SQ SEQUENCE 574 AA: 62977 MW: C179C7085C6F3420 CRC64;

Query Match 16.8%; Score 240; DB 4; Length 574;
Best Local Similarity 28.6%; Pred. No. 1.3e-14;
Matches 69; Conservative 31; Mismatches 93; Indels 48; Gaps 6;

QY 20 GTQSTHESLRP-----QVYQFQSRNFHNLQWOPGRALTGNSSVYVQYKIMFSCSMKSSH 75
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 11 GSUAAHAPEDPSDLLQHKVFOSSNFENILTWDSGEPTD--TVYSIEK----- 58

QY 76 QKPSGCMQHISCNPGGRTLAKYGORQKNEKEDCGTQELSCDLTSETSDIOEPYGRK 135
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 59 -----TYGRDVAKKGCQRTIRKSCNLTVELNLTLEYAVRT 97

QY 136 AASGGSYSEMSMTPTPTWETKIDPPVANNITQVNSLVLIAHNLPRYQKKNVSI 195
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 98 AVSAGGSATMTPTRFSSLSQHTTKLPDVTCTISKVRSIQMIVHPPTPIRAGDGRHLIE 157

QY 196 D-YELLRYRFFIINNSLEKQKVE---GAHRAVEIEALPHSSCYVAELIYQPMIDRR 250
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 158 DIFHDLFHLQVY-----RTYQMHIGKQREFFELPTDTEFLGTIMICVPTWAKE 211

QY 251 S 251
|
DB 212 S 212

RESULT 8
Q99ND6 PRELIMINARY; PRT; 569 AA.
AC Q99ND6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Interleukin-10 receptor, alpha chain precursor.
GN IL-10RA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN (1)
SEQUENCE FROM N.A.
RP TISSUE=PERIPHERAL BLOOD;

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RA Ward H., Vignes S., Poole S., Bristow A.F.;
RT "The rat interleukin-10 receptor: cloning and sequencing of cDNA
RT coding for the alpha-chain protein sequence, and demonstration by
RT Western blotting of expression in rat brain.";
RL Cytokine 0:0-0(0).
DR EMBL; AJ305049; CAC24567.1; -.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor; Signal.
FT CHAIN 17 16 POTENTIAL.
FT SIGNAL 17 569 INTERLEUKIN-10 RECEPTOR.
SQ SEQUENCE 569 AA: 63526 MW: 2354FD6D1B351BD2 CRC64;

Query Match 13.1%; Score 187.5; DB 11; Length 569;
Best Local Similarity 25.1%; Pred. No. 1.4e-09;
Matches 70; Conservative 35; Mismatches 93; Indels 81; Gaps 12;

QY 7 LGFLISFLTVAGQSTHESLKPQVQFQSRNFHNLQWOPGRALTGNSSVYVQYK 64
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 6 LPFLVSISSLSIGFRAHGTELPSPSSWFEARFQHILRMASIPNQ-----SESTY---YE 58

QY 65 IMFSCSMKSHQKPSGCMQHISCNPGGRTLAKYGORQKNEKEDCGTQELSCDLTSETS 124
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 59 V-----ALKYGTSMKDIHICSKAQTLSCLDTTSTL 90

QY 125 DI--QEPYGRVRAASAGSYSEMSMT-PPFTWETKIDPPVANNITQV-----NGSLVI 176
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 91 DLVHSSGYRARRAVDANSQVMTITETRET-----VDEVLTVDSVTVKVSNGFLYGT 144

QY 177 LHAPLNPRYQKKNVSIIDYE-----LVRYRFT-----INNSLEKQKVEGAH 222
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 145 IHPP-----RPNLPVQDESEQITNHRITRYVCIRKPSQKNIITKVQENFTLEVPK 197

QY 223 RAVEIEALTPHSSCYVAELIYQPMIDRRQSRSEECVEI 261
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 198 RM-----RKFCVKVMPHVESRIINKAEMSEQCILHV 227

RESULT 9
Q9YGC8 PRELIMINARY; PRT; 341 AA.
AC Q9YGC8;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Interleukin-10 receptor 2.
GN IL10R2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TaxID=9031;
RN (1)
SEQUENCE FROM N.A.
RP Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster";
RL Genome Res. 0:0-0(1999).
DR EMBL; AF082667; AAD13678.1; -.
DR EMBL; AF082666; AAD13671.1; -.
DR HSSP; P13726; 1AHW.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR001187; Tissue_factor.
DR Pfam; PF01108; Tissue_fac1.
DR PRINTS; PR00346; TISSUEFACTOR.
KW Receptor.
SQ SEQUENCE 341 AA: 39062 MW: 18027239BFA9C87 CRC64;

Query Match 12.6%; Score 180.5; DB 13; Length 341;
Best Local Similarity 24.2%; Pred. No. 3.7e-09;
Matches 56; Conservative 37; Mismatches 97; Indels 41; Gaps 7;

QY 29 KQVQFQSRNFHNLQWOPGRALTGNSSVYVQYKIMFSCSMKSHQKPSGCMQHISCN 88
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

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AC	09YHMO	01-MAY-1999 (T-EMBLrel. 10, Created)	
DT	01-MAY-1999 (T-EMBLrel. 10, Last sequence update)		
DT	01-JUN-2002 (T-EMBLrel. 21, Last annotation update)		
DE	Interferon alpha/beta receptor 1.		
GN	IFNAR1.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LIVER;		
RX	MEDLINE=99177346; PubMed=10077530;		
RA	Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;		
RT	"Comparative genomic analysis of the Interferon/Interleukin-10		
RL	receptor gene cluster.";		
DR	Genome Res. 9:242-250(1999).		
DR	EMBL; AF082664; AAD13669.1; -.		
DR	InterPro: IPR000282; Cytok_receptor_2.		
DR	InterPro: IPR003961; FN_L11.		
DR	SMART; SM00060; FN3; 1.		
KW	Receptor.		
SQ	SEQUENCE 569 AA; 64055 MW; 6A75DDFB891E605 CRC64;		
Query Match	10.9%; Score 155.5; DB 13; Length 569;		
Best Local Similarity	23.2%; Pred. No. 1.7e-06;		
Matches	63; Conservative 38; Mismatches 101; Indels 69; Gaps 12.		
QY	2 PRCFLGLISFFLGVAGTOSTHESLKPORQFOFSRNFHNLQWOPGALGNSSV-YF 60		
DB	224 PLHC-----IKTRKVNLDLCPYIVRVFALNKKFLLMDNH-----NEHYIT 267		
QY	61 VOYKIMFSGSMKSSHQKPGSCWQHISCNPPGCRITLAKYQGRQMKKEDCGTQELSCDIT 120		
DB	268 VOYLIGY--LKNLYDDYSSKWKQVS---GCENT-----SMKCNLS 303		
QY	121 SETSDIOEPYGRVRAASAGSYSEMSMTPRTPMWEKIDPPVYN-----ITQVN 170		
DB	304 SVIKPFSASYFRVQAMN--EYKSKCLSK-----DVEVDPPVTNIEIGPPDYKVVISD-- 353		
QY	171 GSLVYLIAHPNLPYRYQKEKNVSDIDYELLYRPIINNSL--EKQKYEGSAHRAVEIE 228		
DB	354 ---VLHILKITPPGPGPNKIMLS--DLVDFSYQIILYKRNSSDNEEYKMKETKQIATVVS 407		
QY	229 ALTPHSSYCVAAIEIQPMIDRRSORSEECV 259		
DB	408 DLAPSTLYCVKQAFSEAYNKSSDPSREBCI 438		
RESULT 12			
Q9PVJ9	PRELIMINARY; PRT; 442 AA.		
AC	Q9PVJ9;		
DT	01-MAY-2000 (T-EMBLrel. 13, Created)		
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)		
DT	01-JUN-2002 (T-EMBLrel. 21, Last annotation update)		
DE	Interferon alpha/beta receptor 1 (Fragment).		
GN	IFNAR1.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99177346; PubMed=10077530;		
RA	Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;		
RT	"Comparative genomic analysis of the Interferon/Interleukin-10		
RL	receptor gene cluster.";		
DR	Genome Res. 9:242-250(1999).		
DR	EMBL; AF082667; AAD13679.1; -.		
DR	InterPro: IPR003961; FN3; 1.		
KW	Receptor.		
SQ	SEQUENCE 569 AA; 64055 MW; 6A75DDFB891E605 CRC64;		

RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC021825; AAH21825.1; -
DR InterPro: IPR000282; Cytochrome_cytochrome_c.
KW Hypothetical protein.
SQ SEQUENCE 557 AA; 63525 MW; 24A0179DB7F356F CRC64;

Query Match 9.6%; Score 136.5; DB 4; Length 557;
Best Local Similarity 20.8%; Pred. No. 0.00012;
Matches 54; Conservative 39; Mismatches 115; Indels 51; Gaps 7;

QY 2 PKHCFGLISFLTGVAQTOSTHESLKQPVQFOSRNFHNILOMPCGRALGNSSVYEV 61
DB 217 PVHCI-----KTTVENELPPENIEVSQNONVYLKMD---YTYANMTFOV 259
QY 62 QYKIMFSCSMKSHQKPGCGWQHISCNFPGCRITLAKYGQRQWKKEKDCWGTOELSCDLTS 121
DB 260 QWLHAFLEKRNPNH-----LYKKWKOIPDCENVKTTQCVFPQ 295
QY 122 ETSIDIQEPPYGRVRAASAGSYSEMSMTPRFTPMWETKIDPPVMTITQVNGSLVILHAPN 181
DB 296 NVRQ-KGIYLLRYQASDGNSTFSMSEIKFDTEIQAFLLPVENIRSLSDSFHYIGAP- 353
QY 182 LPRRYQKKNVSTIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIHALTPHSSYCVAAE 241
DB 354 -----KQSGNTPIQDYPPIYEITFMENTSNABRKITE-KTQDVTVPNLKRLIYVCYKAR 407
QY 242 IY--QPMIDRRSQRSEREC 258
DB 408 AHMDEKLNKSSVFSDAVC 426

Search completed: December 22, 2002, 10:13:19
Job time : 83 secs

